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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 atgcgcacgcttctgatcga.....ccgtggcgggcgcccgatga 2061
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SUMMARIES
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361.8	365.4	365.4	459	459	478.4	606.2	662.8	701.6	769.8	773	773.4	820	820	1773.8	1773.8	2061	2061	2061	Score	
17.6	17.7	17.7	22.3	22.3	23.2	29.4	32.2	34.0	37.4	37.5	37.5	39.8	39.8	86.1	86.1	100.0	100.0	100.0	Match	21012
55839	2888	2888	4496	4496	300750	298300	110000	29132	138203	39314	4607	4740	2220	14159	2660	5251	2061	2061	Match Length DB	
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AJ586576	AR198353	A48323	AR198356	A48326	AP005217	AP005025	AP006618_17	STH575648	AY310323	SGR300302	STMPABA	SPU60417	AR198361	AF262220	SVU21728	AB116234	BD093914	BD178313	ID	
AJ586576 Xanthomon	AR198353 Sequence	A48323 Sequence 1	AR198356 Sequence	A48326 Sequence 4	AP005217 Corynebac	AP005025 Streptomy	Continuation (18 o	AJ575648 Streptomy	AY310323 Streptomy	AJ300302 Streptomy	M93058 Streptomyce	U60417 Streptomyce	AR198361 Sequence	AF262220 Streptomy	U21728 Streptomyce	AB116234 Streptomy	BD093914 Transform	BD178313 Transform	Description	

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266.8	266.8	266.8	266.8	266.8	266.8	266.8	266.8	267.2	268.2	270	272.2	272.2	272.2	272.2	272.2	278	280.4	282.4	294.6	301.4	307.4	316	317.6	323	335.6
12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	13.0	13.0	13.1	13.2	13.2	13.2	13.2	13.2	13.5	13.6	13.7	14.3	14.6	14.9	15.3	15.4	15.7	16.3
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AX127146 Sequence	BX927151 Corynebac	AP005277 Corynebac	AX764213 Sequence	AX064419 Sequence	AX064177 Sequence	AX121195 Sequence	BD163312 Novel pol	Continuation (27 o	AP003000 Mesorhizo	AE004601 Pseudomon	AR442765 Sequence	AR124158 Sequence	AR099273 Sequence	AR069877 Sequence	A37839 Sequence 9	Continuation (16 o	AL591791 Sinorhizo	Continuation (31 o	M83788 Haloferax v	AP005045 Streptomy	Continuation (13 o	CQ363747 Sequence	Continuation (22 o	AL939115 Streptomy	AL939111 Streptomy

ALIGNMENTS

Query Match	FEATURES SOURCE			COMMENT		VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 BD178313 LOCUS DEFINITION ACCESSION 1
th 100.0%; Score 2061; DB 6; Length 2061;	rendering the same CC and novel biosynthetic gene FH Key Location/Qualifiers FT CDS Location/Qualifiers 12061 /organism="Streptomyces venezuelae" /mol_type="genomic DNA" /db_xref="taxon:54571"	2N1/15,C12P17/14//(C12N1/15,C12R1:645),(C12P1	PN WO 02077244-A/1 PD 03-CCT-2002 PF 22-MAR-2002 WO 2002JP002782 PR 22-MAR-2001 JP 01P 082227 PI KOJI YANAI,NAOMI SUMIDA,MANABU WATANABE,TATSUKI MORIYA,TAKESHI	PALENI: WO 02077244-A 1 03-0CT-2002; MEIJI SEIKA KAISHA LTD,KOJI YANAI,NAOMI SUMIDA,MANABU WATANABE, TATSUKI MORIYA,TAKESHI MURAKAMI OS Streptomyces venezuelae	Yanai,K., Sumida,N., Watanabe,M., Moriya,T. and Murakami,T. Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene	BD178313.1 GI.30015578 WO 02077244-A/1. Streptomyces venezuelae Streptomyces venezuelae Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 2061)	2061 bp DNA linear PAT 16-APR-2003 Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene.

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1021 GCCGACCGCGCATCGGCCTCGACCACCAGGAAGGCTGCTGCTGCTGCTGGCCCTCGAC 1080	961 GCGGAGACCACCGGCGACCCCGCGCACCCGGTCCCCGCACCCCGACGCCGCGTTCCTCTTC 1020	901 CCCGAACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCGGCTACGAGCTGAAG 960 	841 CGGCGCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGACGGGTCCCCGTCGCC 900	781 TACCGCGTCGCCGACGGCGTCGTCCGCTCCGCGGCTCCGACGCACCACGACCCGGACG 840	721 GGCGCCTCGCGCTTCCTCGGCCGACGACCGCCGCCCCCTCGCCCAGCTACCTCACC 780	661 CGCGGCTGCCTGCCCGGCGAGGGCACCACGTTCTGGCTGG	601 TCCCCGTACGAACTCCACGTGCGCCGCGTCGACGTGCTGCCGGACGCCCGAAGAGGTACGC 660	541 ATGGCCAACTTCCGCGACCTCGCCCTCGCCCACCACCACCGGGACGGCGCCACGGGGCCACGGGGCCGACGGGCCGACGGGGCCGACGA	481 CCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGAGCTTCGGCCGGGAGATC 540	421 CTCGAACCCCTCGCCTGGAGGACGACGACGGGTCGTCATGGGCCTGCGGCACCGCGAGAAG 480	361 CCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTGGCCGCCACCGACCTCCCCGACGAG 420	301 CCCATGCACGGCCGGGTCTCCGAGGTGCGGCACACCGGCGAGGACGTCTTCCGGGGCCTC 360	241 TGCCTCGGCCACCAGGGCATCGCCCAGCTCTTCGGCGGAACCGTCGGCCTCGCCCCGGAA 300	181 CGGGACTTCGGAATCAGCCGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCGGCGTC 240	121 CCCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCAGCCCCGACCGGGAA 180	61 GGCGAGGCCACCGGGCAACCCCCCGTCGTCGTGCCCAACGACGCCGACTGGTCGCGGCTG 120	1 ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGTACATC 60	Best Local Similarity 100.0%; Pred. No. 2.2e-158; Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 2 BD093914	2041 GCC Db 2041 GCC	1981 GA	1921	1861	1801	1741 1741	Qy 1681 GCC Db 1681 GCC	1621	1561	1501	1441	1381	1321	1261	1201	1141	1081	Db 1021 GCC
	CGTGGCGGCGCCGATGA 2061	HILLING CONTROL OF THE CONTROL OF TH	SCGARTICGECGICGECGGGGCAITCGIGTCCCTCCGACCAGAGA	CATCGTGCTG 192	ACCATGGACATCATGGACGCCTGGAGGAAGGCCCCCGGGGCGTCTACTCCGGGGCGCTC 1860	180	GCGCCCGTGCACCACCTGCTGTCCACCATCAGGGGACGCCTGCGGCCCGGCACCAGCACC 1740		سر سر ،	. <u>, , , , , , , , , , , , , , , , , , ,</u>		<u> </u>	138				1 1	GCCGACCGCCATCGCCTCGACCACCAGGAAGGCTGCTGCTACCTGCTGGCCCTCGAC 1080

9	B &	D QV	 B &	B 8		D Q	Db Qy	Query Match Best Local Simil Matches 2061; C	ORIGIN	FEATURES			COMMENT	TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION
421 CTCGAACCCCTCGCCTGGAGCGACGACGGGGTCGTCATGGGCCTGCGGCACCGCGAGAAG 480	361 CCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTGGCCGCCACCGACCTCCCCGACGAC 420	301 CCCATGCACGGCCGGGTCTCCGAAGGTGCGGCAACACCGGCGAGGACGTCTTCCGGGGGCCTC 360	241 TGCCTCGGCCACCAGGGCATCGCCCAGCTCTTCGGCGGAACCGTCGGCCTCGCCCCGGAA 300	181 CGGGACTTCGGAATCAGCCGCGGGGGATCACCGACAGCGGCCTGCCCGTCCTCGGCGTC 240	CCCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCAGCCCCGACCGGGAA	61 GGCGAGGCCACCGGGCAACCCCCCGTCGTCGTGCCCAACGACGACTGGTCGCGGCTG 120	GCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGI	ch 100.0%; Score 2061; DB 6; Length 2061; 11 Similarity 100.0%; Pred. No. 2.2e-158; 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		FH Key Location/Qualifiers FT CDS (1)(2058). Location/Qualifiers	MIYAMOTO, NAOKI MIDO, TAKESHI MURAKAMI C12N15/09,C12N5/10,C12P21/02,C07K11/00//(C12P2		MEIJI SEIKA KAISHA LTD,KOJI YANAI,KAORU OKAKURA,SHOHEI YASUDA, MANABU WATANABE,KOICHI MIYAMOTO,NAOKI MIDO,TAKESHI MURAKAMI OS Streptomyces venezuelae PN WO 0127442-A/1	Transformants that produce secondary metabolites modified by a functional group(s) and novel biosynthesis genes Patent: WO 0123542-A 1 05-APR-2001;	Bactearia; Actinobactearia; Actinobactearidae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 2061) Yanai,K., Okakura,K., Yasuda,S., Watanabe,M., Miyamoto,K., Mido,N.	BD093914.1 GI:22639502 WO 0123542-A/1. Streptomyces venezuelae Streptomyces venezuelae	BD093914 2061 bp DNA linear PAT 27-AUG-2002 Transformants that produce secondary metabolites modified by a functional group(s) and novel biosynthesis genes. BD093914
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1501 GGCCGGGAGAAGGACCGGGCCGAGAACCTGATCGTCGACCTGGTCCGCAACGACCTC 1620	41	81 ATCAGCCCCGTCCCGTACGGCGCCCTGCTCGAGTTCCCCGAACTGTCGGTGCTGAGCGCCCTGCTCCGTACGGCCCCTGCTCCGAGCTTCCCCGAACTGTCGGTGCTGAGCGCCCTGCTCGAGCGCCCCGAACTGTCGGTGCTGAGCGCCCAACTGTCGGTGCTGAGCGCCCAACTGTCGGTGCTGAACGATCCCGAACTGTCGGTGCATGAACGATCAACGATGAACGATGAACGATGAACGATGAACGAAC		61 CGCATCGACGAGTGCCTCAAGGAGATCCGCAACGGCGAGTCGTACGAGATCTGCCTGACG	01 GCGGCGGCCTCCGCCCCTGGCCCCGCGCGCGCACGACAAGGACGCCTACCTCAAG	1141 GGCCTGGCCGTCCGGCCCCGGCCGAGCCGACCCCCGCCATGGTCTTCGGGATCCCCGAG 1200 1141 GGCCTGGCCGTCCGGCCCCGGCCGAGCCGAGCCCCGCCATGGTCTTCGGGATCCCCGAG 1200	B1 CGCCGGGGCCACGACGACGGCGCCCGGGCCTGGCTGGGGGAGACGCCGAGACCCTCACC	21 GCCGACCGCCCATCGCCCTCGACCACGAAGGCTGCTGCTACCTGCTGGCCCTCGAC	961 GCGGAGACCACCGGCGACCCCGCGCACCGCGCACCCCGACGCCGC	901 CCCGAACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCGGCTACGAGCTGAAG 960 	841 CGGCGCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGACGGGTCCCCGTCGCC 900	781 TACCGCGTCGCCGACGGCGTCGTCTCCGTCCGGCGCTCCGACGGCACCACGACCCGGACG 840	721 GGCGCTCGCGCTTCTCCTCGGCGACGACCGCGGCCGCGCTCGCCGAGTACCTCACC 780	661 CGCGGCTGCCCGGCGAGGGCACCACGTTCTGGCTGGACAGCAGCTCCGTCCTCGAA 720	ol TCCCGTACGAACTCCACGTGCGCCGCGTCGACGTGCGCGGACGCCGAAGAGGTACGC	ATGGCCAACTTCCGCGACCTCGCCCTCGCCCACCACCGGCACGGCGCGACGACGACGACGACGACCACGGCACCAC	481 CCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCGGCCGGGAGATC 540

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                                                                                                                                 Submitted (01-AUG-2003) Koji Yanai, Meiji Seika Kaisha, Microbiological Resources and Technology Laboratories; Odawara-shi, Kanagawa 2500852, Japan (B-mail:koji yanai@meiji.co.jp, Tel:81-465-37-5106, Fax:81-465-37-6397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB116234 SZ51 bp DNA linear BCT 03-JUI Streptomyces venezuelae papA, papC, papB, ORFIV genes for 4-amino-4-deoxychorismate synthase, 4-amino-4-deoxyprephenate dehydrogenase, 4-amino-4-deoxychorismate mutase, hypothetical
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RESULT SVU2172	D Q	g Q	da Vo	g dg	g Vy	dg VQ	Db Qy	Qy	dg VQ	Qy du	dg . Qy	B &) b Q	₽ \$	} B 5	?	Q dd)
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DNA linear		GCCATGGTCACCGCC	GCGATCGTGTCCCTC	AGCATCGTCATCCGC AGCATCGTCATCCGC	CCCCGGGGCGTCTAC	TCCATGACCGGCGCC	GGACGGCTGCGGCCC	CCCCGGCTCTTCGAC	;ATCGTCGACCTGGT(ATCGTCGACCTGGTC	GACGAGCGGCTCCGC	GGCGGCGTCGAGTC	HICCCCGAACTGTC	CTGCCGCTCTACTC	GGCGAGTCGTACGA	CGCCACGACAAGGA	CCCGCCATGGTCTTC	CTGCGGGAGACGGC	
BCT 22-NOV-1		CTCGACGGCACCGCAC	TCCGACCAGG	ACCATCGTGC	Trcceeeecec	CCCAAGAAGC	GGCACCAGCA GGCACCAGCA	GTGGAGACCT	CGCAACGACC CGCAACGACC	GCCGACCTGG GCCGACCTGG	CAAGCCCATCA	GGTGCTGAGCG		GATCIGCCIGA	CGCCTACCTCA	CGGGATCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGAGACCCTCA CGAGACCCTCA	

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Query Match 86.1%; Score 1773.8; DB 1; Length 2660; Best Local Similarity 92.8%; Pred. No. 3.2e-135; Matches 1913; Conservative 0; Mismatches 97; Indels 51; Gaps 3; 1 ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGTACATC 60	/ COUNT SCRIFE - 1 / (Transi Lable = 11 / product = "paminobenzoic acid synthase" / product = "paminobenzoic acid synthase" / protein id = "AAB30312.1" / protein id = "AAB30312.1" / db xref = "gi.710438" / gi.710438" / gi.710		/or /mc /db /oc /nc /tr	က စ	Complete cds. Complete cds. U21728 U21728.1 GI:1680048 Streptomyces venezuelae Streptomyces venezuelae Streptomyciaeae; Streptomycetales; Actinobacteria; Streptomyces. 1 (bases 1 to 2660) 1 (bases 1 to 2660) 1 A role for pabAB, a p-aminobenzoate synthase gene of Streptomyces venezuelae ISP5230, in chloramphenicol biosynthesis Microbiology 142 (pt 6), 1345-1355 (1996)
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Streptomyces venezuelae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                      Streptomyces venezuelae partial sequence. AF262220
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The gene cluster for chloramphenicol biosynthesis in Streptomyces venezuelae ISP5230 includes novel shikimate pathway homologues and a monomodular non-ribosomal peptide synthetase gene microbiology 147 (Pt 10), 2817-2829 (2001)
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Sequence update by submitter
On Jun 5, 2001 this sequence version
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Direct Submission
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Direct Submission
Direct Submission
Submitted (11-JUN-1996) Recherche F
Submitted (11-JUN-1996) Recherche F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4740 bp
Streptomyces pristinaespiralis 4
precursor biosynthesis (papA, pa
                                                                2 (bases 1 to 4740)
Blanc, V., Gil, P., Bamas-Jacques, N.,
Bisch, D., Blanche, F., Debussche, L.,
                                                                                                                                                                                                                                                                                                                                              Streptomyces pristinaespiralis
Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Acti
                                                                                                                                                                   Identification and analysis of genes from Streptomyces pristinaespiralis encoding enzymes involved in the biosynthesis of the 4-dimethylamino-L-phenylalanine precursor of pristinamycin I Mol. Microbiol. 23 (2), 191-202 (1997)
                                                                                                                                                                                                                                                                 Blanc, V., Gil, P., Bamas-J. Schleuniger, J., Bisch, D.,
                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (papA, papC, papB,
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4-dimethylamino-L-phenylalanine
papC, papB, papM) genes, complete
            Pharmaceutique, Rhone-Poulenc . 14, Vitry sur Seine cedex 94403,
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                                                                  Lorenzon,S.,
Crouzet,J. a
                                                                    ., Schleuniger, J., and Thibaut, D.
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887 GGGTCCCCGTCGCCCCGAACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCG 946	827 CCACGACCCGGACGCGGCGCCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGAC 886	767 CCGAGTACCTCACCTACCGGCTCGCCGACGGCTCTCCGTCCG	707 GOTOCGTCCTCGAAGGCGCCTCGCGCCTTCTCCTTCCTCCGACGACCGAC	647 CCGAAGAGGTACGCCGGGGCTGCCTGCCGGCGAGGGCCACGTTCTGGCTGG	605CGTACGAACTCCACGTGCGCCGCGTCGACGTGCCGGACG 646	561	536 AGATCATGGCCAACTTCCGCGACCT560	476 AGAAGCCGCTGTGGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCCAGC	416 ACGAGCTCGAACCCCTCGCCTGGACGACGACGGCGTCATCGGCCCTGCGGCACCGCC 475	356 GCCTCCCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTTGGCCGCCACCCGACCTCCCCG 415	296 CGGAACCCATGCACGGCCGGGTCTCCCGAGGTGCGGCACACCCGGCGAGGACGTCTTCCGGG 355	236 GCGTCTGCCTCGGCCACCAGGCATCGCCCAGCTCTTCGGCGGAACCGTCGGCCTCGCCC 295	176 GGGAACGGGACTTCGGAATCAGCCGGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCG 235	122 CCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCCAGCCCCGACC 175	62 GCGAGGCCACCGGGCAACCCCCCCGTCGTCGTCGCCAACGACGCCGACTGGTCGCGGCTGC 121	2 TGCGCACGCTTCTGATCGACACTACGACTCGTTCACCCACAACCTGTTCCAGTACATCG 61	Natch 39.8%; Score 820; DB 1; Length 4740; Local Similarity 64.4%; Pred. No. 3.2e-58; Les 1356; Conservative 0; Mismatches 655; Indels 93; Gaps 5;	DGCLTAVRNHTCAPPA"
																		
dg dg	B &	, B &	S & &	B &	B &	\$ \$ \$	ρ ξ	, B &	\$ B &	, B &	B &) B () B (S B &	5 B 7	S B &	. B 8	ָ מם
1967 TCTCCGACCAGGAGGAGGAGTTCACCGAGACCGTGGTAAAGGCCCGCGCCATGGTCACCG 2026	GCACCATCGTGGCTGGCGGGGGGGGGATCGTGTCCC	80	20	60 2		6 6	80	620	60	00 5	40	90 1	20	60	15	155	95	35

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COMMENT
FEATURES
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DEFINITION
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MEDLINE
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TITLE
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pab gene.
Streptomyces griseus
Streptomyces griseus
Streptomyces griseus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Streptomyces :
M93058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 4007).
Criado, L.M., Martin, J.F. and Gil, J.A.
The pab gene of Streptomyces griseus,
synthase, is located between genes por
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Original
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1 (bases 1 to 4607)
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FQVETYATVHQLVSTVTARLREDSSPVAAVRAAFPGGSMTGAPKIRTMQIIDRLEGGP
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                                                                                 APLLRLLDTAFPGRERPGKDLDGEPDDGTDAGAPKDLVLPG"
                                                                                               {	t RGVYSGAIGYFSLTGAVDLSIVIRTVVLSGGRLRYGVGGAVIALSDPADEFEETAVKA
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/product="p-aminobenzoic
/protein_id="AAA72111.1"
/db_xref="GI:388263"
                                                                                                                                                                                                                                                                                                                                           /gene="pabAB"
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/mol_type="unassigned DNA"
/db_xref="taxon:1911"
                                                                                                                                                                                                                                                                                                                             /gene="pabAB"
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                                                      note="p-coumarate:CoA ligase homolog"
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 CGGACGCGCGCCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGACGGGTCCCC
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/translation="MVPVHAHDYVTDPPSTTGRTLDGLTLPRVFADAVHRGGDAVALV
DGEYALTWSAWRTAVDALARGLQBSGVVSGDVVALHLPWSWELLTLHLLAASVGAVTM
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GBGTETVTEMLERWSGEDPLPVEVRPDSPFLLLPSSGTTSARPKICLHSHEGLLTVNS
GBGTETVTEMLTRAVGGEDLTPVEVRPDSPFLLLPSSGTTSARPKICLHSHEGLLTVNS
AATEDTADAYAGTLITACPLTHCFGLQSAYSALFRAGRQVLLSGWDVGRFLELARRER
AATEDTADAYAGTLITACPLTHCFGLQSAYSALFRAGRQVLLSGWDVGRFLELARRER PSVVVAVPASCTTWSPGCARTRTAPASARPDP"

1550 CCGGCCGACTTCGGCCTGTGCGCCCGGATCGCCGAGGAGGGCCGGCTGCCGGGTGCTCGGC GCCAAGGCCGACGTGCACGCCGGAACCGTCACGGTGAGAG----CCGACGGCGCCAGCAGC CTCGAAGGCGCCTCGCGCTTCCCTCGGCGACGACGGCGGGGCCCGCTCGCCGAGTAC ATCATGGCCAACTTCCGCGACCTCGCCCTCGCCCACCACCGGGCACGGC------GAACCCATGCACGGCCGGGTCTCCGAGGTGCGGCACACCGGCGAGGACGTCTTCCGGGGC CTCACCTACCGCGTCGCCGACGGCGTCGTCTCCGTCCGCGCGCTCCGACGGCACCACGACC GGGGGCGAGCTGGGCCAGCTCTCCATGATGGGCGACGCCTCAGGTCCCCTCGCCCGGACC GCCTTCGACTCGCTGTTCCGCACCGGCGACCACCCCTTCTGGCTCGACAGCAGCCGTCCC ACCCCACGGGGGCTCCGGGTCATCGCCAAAGTCGCTGCCCACGCGCTGGGACGCCGAGGTC GCGTCGACGTGCCC-----CTGCTGGCCAACTTCCGCGACCTCACCGAGCGCCACGGCCGAACGCGCCACGGCGGCCGG AAGCCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCGGCCGGGAG GAGCTGGAGGCCACCGCCTGGTCGGAGGACGGGGTCCTGATGGCGCCTGCGCCACCGCACG GAGCTCGAACCCCTCGCCTGGAGCGACGACGGGGTCGTCATGGGCCTGCGGCACCGCGAG CTGCCGCAGCCGCTGGAGGTGGTGCCGCTACCACTCCCTCGCGGTGACGGAACTGCCGCCG CTCCCCTCGCCGTTCACCGCCGTGCGCTACCACCTCCCTGGCCGCCACCGACCTCCCGAC GAGCCCCGTCACGCCACCTCGGCGGTACGGCACGACGGCACCGGGCTCTTCGAGGGG GTCTGCCTGGGCCACCAGGGCATGGCCCTCGCCCACGGCGCCCGGGTGGGCCGGGCCCCC GAACGGGACTTCGGAATCAGCCGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCGGC GGTCTGCTCGACGCGTTCGACAACGTGGTGCTCTCCCCGGGGGCCGGCACCCGCACCGC CTGCCCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCAGCCCGACCGG TCCCGGGCCAACGGCCGGGAACCCGAGGTCATCCGCAACGACGACCGGCCTGGCGGCCG GGCGAGGCCACCGGGCAACCCCCCGTCGTCGTGCCCAACGACG----CCGACTGGTCGCGG ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGTACATC ATGCGCACCCTTCTCGTCGACAACTACGACTCGTTCACCTACAACCTCTTCCACTACCTC Conservative GTGGGGAGTGCAGTTCCACCCCGAGTCGATCGGCACCCAGGACGGCCACCGG 37.5%; 0; Score 773.4; DB 1 Pred. No. 1.9e-54; Mismatches 686; 1: Indels Length -GGACGCCGAAGAG 4607; 96; Gaps 1969 477 2266 834 2209 2089 2029 1909 537 1729 774 2149 714 654 625 586 1849 1789 417 1669 1549 1489 357 297 1609 237 177 117 1429 60

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Streptomyces griseus partial ORF1, cant gene, cant gene and cantB gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spain
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                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic
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                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                            organism="Streptomyces
                                                                                                                                                                                                                                                                                                                                                     _xref="taxon:1911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Gil, J
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Streptomyces griseus
Streptomyces griseus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14:NOV-2000) Gil J.A., Microbiologia,
Leon, Campus de Vegazana s/n, 24071, SPAIN
Location/Qualifiers
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8 (Pt 1), 51-59 (2002)
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W"
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Best Local Similarity
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CORGANISM
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Chen,S., Huang,X., Zhou,X., Bai,L., He,J., Jeong,K.J., Lee,S.Y. and Polyene Complex
Chen,S., Hopolational and Mutational Analysis of a Complete
FR-008/Candicidin Gene Cluster Encoding a Structurally Related
JOURNAL Chem. Biol. 10 (11), 1065-1076 (2003)
AUTHORS
Chen,S., Huang,X., Zhou,X., He,J., Bai,L., Jeong,K.J., Lee,S.Y. and
Direct Submission
Direct Submission
Streptomyces sp. FR-008
Chen,S., Huang,X., Zhou,X., He,J., Bai,L., Jeong,K.J., Lee,S.Y. and
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Streptomyces sp. FR-008
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Direct Submission
Streptomyces sp. FR-008
Chen,S., Huang,X., Zhou,X., He,J., Bai,L., Jeong,K.J., Lee,S.Y. and
Submitted (30-MAY-2003) Bio-X Life Science Research Center,

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FEATURES
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China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4377. .7205)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3150. .3818)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSTIPLASRLYLSRQGVEYHVTGLLRKLKVPNRAALVSRAYSMGVLKVGTWPPKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3150. .3818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MIELDGEPAGPEALASLALTNYGHFTTLLVENGRVRGLDLHLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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LEGYHAARGPVGTAMVGLARRMGSAQVEETPDWSAMGQAEFDAWWQEQNNGSDRRSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTAPPRIDGLHPDLRTPTSLPPGRLNAELTEHLRALVAEHFPPFWAAKLLSTPAETTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (574. .1950)
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gene

CDS

gene

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PPGPHVPSAVARPPGPRPAVLTGRRTAKAPGHDAAVWHGLTAVERETAALAAQGLGNR
EIATELAVTTRAVELRLSGVYRKLRIRGREELRALVQEAEGS"
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ANALVHIEQALVHLGGRELAQAREGSETALGWTEPAHQGLDTAATMTHAIVALLESDEY
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VRPWTDAMCGAVALAQTERLDEILATRREIEARYDAGLKDLPGITLMPARDVLMWYDLR
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STREPTONYCES THIOLUTEUS
Bacteria; Actinobacteria; Actinobacteridae; Actinobacteria; Actinobacteria; Actinobacteria;
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AJ575648.1 GI:41322765
AJ575648.1 GI:41322765
acyl-coA ligase; aurA gene; aurB gene; aurC gene
gene; aurF gene; aurG gene; aurH gene; aurI gene
gene; aurF gene; transferase; PABA synthase;
type I; transcriptional regulator.
                                                                                                                                                                                                                                                                                                                   Iteration as programmed event during polyketide assembly; molecular analysis of the aureothin biosynthesis gene cluster Chem. Biol. 10 (12), 1225-1232 (2003)
                                                                                                                                                                                              Submitted (07-JUL-2003) Hertweck C.,
Hans-Knoell-Institute, Beutenbergstr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STH575648 29132 bp DNA line Streptomyces thioluteus aureothin biosynthesis (aurABCDEFGHI genes), strain HKI-22.
                                                                                                                                                                                                                                                        Direct Submission
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gene; cytochrome P450;
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Pred. No. 5.7e-49;
3; Mismatches 697;
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Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(and Satoshi Omura(*1,*3). Final finishing process and all annotation were done and J. Ishikawa. *1 Kitasato Institute for Life Sciences, Kitasato *2 National Institute of Infectious Diseases *3 The Kitasato Institute *4 National Institute of Technology and Evaluation *5 School of Science, Kitasato University *6 Institute of Medical Science, University of Tok *7 RIKEN, Genomic Sciences Center *7 RIKEN, Genomic Sciences Center Following url is also available. http://avermitilis.ls.kitasato-u.ac.jp. Location/Qualifiers source /organism="Streptomyces avermitilis MA-4680"	Direct Submission Submitted (29-MAR-2002) Director-General of Biotechnology Cent. National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424) This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayn Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomoolosnoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tomoolosnoe(*4), Hisas	12692562 3 (bases 1 to 298300) 3 (bases 1 to 298300) Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Takahashi,Y., Horikawa,H., Nakazamashinose,M., Director-General of Biotechnology Sakaki,Y. and Hattori,M.	Keda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuo Shiba, T., Sakaki, Y., Hattori, M. and Omura, S. Complete genome sequence and comparative analysis of microorganism Streptomyces avermitilis Nat. Biotechnol. 21 (5), 526-531 (2003) 22608306	1680 1600 1600 1600 17 18 19 19 19 19 19 19 19 19 19 19 19 19 19	Db 52272 CTCGGCGGCACCGCCGACCATCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT
attori(*1,*7) gene e done by H. Ikeda tasato University CDS luation of Tokyo	E Biotechnology Center, ation, Biotechnology o 151-0066, Japan .nite.go.jp/, aruo Ikeda(*1), Jun a Takahashi(*3), Mayumi 1 Nakazawa(*4), Tomomi i Nakazawa(*4), Tomomi	Takahashi,C., va,H., Osonoe,T., Center, Shiba,T.,	is ×	gene es. Takahashi,C., Takahashi,C., a,H., Osonoe,T., streptomyces y secondary 12220 (2001)	GCGGCACGACGGCGC 52213 GCGGCACGACGGCGC 52213 GGAGGAGGAGTTCACC 1992 G

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979. .2217
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208. .921
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                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3187. .4086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARSRPLPAGRRPPRPWPAASA"
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/protein_id="BAC68656.1"
/db_xref="GI:29604587"
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                                                                                                                                                                                                                                                                                                 /gene="aveBIII"
/note="SAV947
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/transl_table=
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/note="SAV944
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/strain="MA-4680"
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/note="SAV945
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note="This strain is also named as strain: ATCC 31267,
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Query Match
Best Local Similarity
Matches 1262; Conserv
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                     Conservative
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/product="dTDP-6-deoxy-L-hexose 3-0-methyltransferase"
/protein_id="BAC68661.1"
/db_xref="GI:2960450""
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ELARMPVLLRLVARRPGVVPPGGASAETETTADLTAASSVALAAVTDADVIHLVVARLT
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GEPDEPVTAYARQKLDAERTIKSATVEGVLRGISLRLFTVYGAGPGPQCMGVVQAMVL
RALADEALTVMNGSVVERDLVHVEDVAQAFVSCLAHADALAGRHWLLGSGRPVTVPHL
                                                                                                                                                                                                                             complement (7442. .8215)
/gene="aveBVII"
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                                                                                                                                                                                                                                                                                                       LTRRIGGVPHLLAHGRVEGGFLDTIELGPTVQYTPRNYAHLTGPARPRFLDLVLEAAP
DRIRYAAVHSEEGGRFLHAQARYLFVEADESQAPNDPPPGYRWCTPGQLTQLLRYGRY
VNVQARTLLSLLTTRAVEL"
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ARGRALDFVVDLRTGSPTFGQMDSVLLDQERFRSVYLDFIGVGHAFVALEDTAMVYLM
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/product_"dIDP-4-keto-6-deoxy-L-hexose 4-reductase"
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/db_xref="GI:29604589"
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4212. .5243
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4212. .5243
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FTWLDAGTHDSLMHAGQYVQVLEKRQGVRIACLEEIAFRMGLIDADDCYLRGVELAGS
                                                                                                                                                                                                               /note="SAV951
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/transl_table
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/protein_id="BAC68659.1"
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/note="SAV948
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Pred. No. 1.1e-41;
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                                         GACTGCCGTTCGACTTCACCGGCGGGTATGTGGGCTACTTCGGCTACGAGGTGAAGGCCG
                                                                          AACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCGGCTACGAGCTGAAGGCGG
                                                                                                               CCAGCGTCTTCGACTACCTGAAACGGCAGTTGGTGACCCGTCAGGT---GGATGCCACGG
                                                                                                                                                  GCCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGACGGGTCCCCGTCGCCCCG
                                                                                                                                                                                           GCGTCGCCGACGGCGTCGTCCCGTCCGCGGCTCCGACGGCCACCACGACCCGGACGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-Kw. Tokyo 151-066, Japan (E-mail:bio@nite:go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukub
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                                                                                                                                                                                                                                             /translation="mDQAPSGCLVDCVHGYIFYDTPVPMLLFPVGTSGNRKIVLDLFNHTHVYVCVVFCGEFDPGSGRTLAAC
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/strain="YS-314"
/codon_start=1
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/db_xref="GI:23492723"
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Ikeo, K.
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/translation="mpcfpfsqirqtkytstapklgdimkkdspypttttgwleqlddd
QLSGilrnrpdtalplppglgslaarlqlrasiqrayhklsalelayleaaanagael
Npitapeyverhralrhslayptaeqigealnrlrqlalvfggerfiilpetmatlp
                                                                                                                                                                                                                                                                                                          complement (9548. .11851)
/note="CE0892, similar to AE006976-11|AAK45126.1|
                                                                                                                                                                                                                                                                                                                                                         LAATAHTKTRVVRRILEQHQGQPTLIIGAYLDQLEELGAEFDAFIVDGKTSNKKRGEL
FDRERSGELNVLVVSKVANFSIDLPEAAVAIQVSGTFGSRQEEAQRLGRLLRPKADGG
EAHFYSVVSRDTLDTEYAARSRFLAEQGYAYRIIDADDLLFFITEKET"
                                                                                                                                                                                                                                                                                                                                                                                                                                          VHTYRITPLALMNARAAGHDAEQVVDVLERYSRFPVPQPLLVDVAETMSRYGRVRMHK
HPAHGLILESSEPAILVEISRHRKIKPMLGQQLDFETIAVHSEERGRLKQELLKIGWP
AEDLAGYVDGEAHPIALSTEVEDWSLRDYQQADADSFWEGGSGVVVLPCGAGKTMVGA
ASMARAQATTLILVTWTVAGRQWKDELLRRTTLTEDEIGEYSGERKEIR PVTLATYQV
VTRRTKGEYKALELFDSRDWGLIYDEVHLLPAPVFRMTSDLQSRRRLGLTATLVRED
GREGDVFSLIGPKRYDAPWKDLEAQGFIATADCVEURTTMTDAERMVZATAETADRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7822. .9495)
/note="CE0891, similar to AL583924-93|CAC31112.1| percent
identity: 75 in 547 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="withesedvdeayarknnselrdtkrlqisafefejlyllaiggyl
yyllaganwgwwyli'nwgiwalseywi pylergygsasslynysplyeayvasinpr
dyyllalynynydetleprwglayetinrigyndhdrklgeryesyaysgratiroqdhw
deisempitwgttdadvyrraektiphdlwnkleknrnrldevkntrwnllyl"
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pmleiasQqilggnnqysggrgdlglrtavasdrhkrfkldydpdtevlitvgateai
sasvlglvepgdevivlepyydayaaialagatrvavplkeedntwvldtdavhaav
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                               TNWQLLPEEHGRSLTFGEASQSIEALPARHRKILVTLVTSNGLGLTRDAALSADPARP
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VAHAVAHEKFWVKQMRKGLQNKRDILTDALTQAGLKVHDSHGTYFVVADIGERDGAEF
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NNPPHEHSPWWVY"
                                                                                                                                     /product="conserved hypothetical protein"
/protein_id="BAC17702.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative DNA helicase"
/protein_id="BAC17701.1"
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/translation="MAFGDGPLIVQSDKTVLLETGHDLAGEARAALAPFAELERAPEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical
/protein_id="BAC17700...
/db_xref="GI:23492728"
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/protein_id="BAC17699.1"
/db_xref="GI:23492727"
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/product="58 ribosomal RNA"
/note="CErRNA03"
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identity: 79 in 387 aa"
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     PQLIKAGLLSRVDEQTVKLPGVVRRVLEGQEDTAWRVVPVEPSAVPGADDAGIAAGI
                                                                                                                                                                                                                               codon_start=]
transl_table=
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                                                                                                                                                                                                                                                                                dentity: 36 in 741 aa"
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Matches 1164;
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                                                       184949 AGGAGGTCACCGGTGCGGCACCGACGGTGCTGCCCAATGATG-----
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                        184889
122 CCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCAGCCCGGCACCGGGAAC 181
                                                                                                              62
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SdD

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GCGAGGCCACCGGGCAACCCCCCGTCGTCGTCGCCCAACGACGCCGACTGGTCGCGGCTGC
                                                                                                        TGCGCGTACTGATCGACAATTATGATTCCTTCACCTTCAACCTCGCCACGTATGTGG
                                                                                                                                            TGCGCACGCTTCTGATCGACAACTACGACTACGTTCACCCACAACCTGTTCCAGTACATCG
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                      complement (14424. .15254)
/note="CE0897, similar to AE001874-1|AAF09704.1| percent identity: 40 in 267 aa"
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RRGVPDPLPADDGGDYIAFPPVÅDEWLQATILÆGLAHLMRGWMYQTVAAWLVGEADE
KNKPIHLLSPASRRDALPETRAMÍLQSIKJRVEGEADLFFHHPLAASIPRETIRH
LLEEBARWIGAVAGGGVTSPARVLTQAPAGVIPEIADIAVARPKPUDAFTIVA
MVPGPLQPEMQKIIGQLADLESPGLASVYRISEASLRHAMDLGLTATEIEDFLTQHSA
TGLPQSVAYLLQDIARRHGTLRGGPALCYLRSDDPALLHSAVEAAGALGLRQIAPTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="masrktkrkkifiqiathlyavvvvvvisvvfqnwmnnrpepepe
TVSITASSPAGEIEVFPYSICEPGVECAENEVPTLEVGADEELRLTIPEIIHDHDWYL
LTIYDDPAANDEFYHTSYETTEVTVPGSVDPVTEGGERPRLVVVEVTSVMIGTDDNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="mpvGTvKwydpeRGFGFvSnpGGEDCFvGKQVLpKGvTELHQGQ
RIEFDFAAGRKGPQALRVKVLETÞRRRPQHTYKPEELNGIISDMVTMLEGTVQPALLK
GHYPDRKVGEQVAKILRAVAKELĖA"
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drlancesggnwaintgngyhggi,qfspstwrayggdefapfayqatreqqiavaert
lagqgwgawpacssklglnsa.ptbrnlnpapapapapaapaeyratvdtntnpvvgss
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                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
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/note="CE0894, similar to AX133781-1|CAC38957.1| percent
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AVAAI RREEVARTGTVSDQPTLAVLQAAVRGQRTVTLGFVDKQGVAVHRTVKPLTVNA
                                                                                                                                                                                                                                                                                                                    /product="putative glutamine cyclotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETPYTTTWSLATVEQ"
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/product="hypothetical protein"
/protein_id="BAC17706.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (13881. .14408)
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/protein_id="BAC17705.1"
/db_xref="GI:23492733"
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/note="CE0895,
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/protein_id="BAC17704.1"
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/protein_id="BAC17703.1"
/db_xref="GI:23492731"
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/product="conserved
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0; Mismatches
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n 62 aa"
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ches 676;
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                                                                                                                                                                                                                                                             Length 300750;
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-CGCAGATCG 184999
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962 CGGARACCACCGGCGACCCCGGCACCCCGACCCCGACGCCGTTCCTTTCG 1021	182 GGACTTCGGANTCAGCGGGCGGGGGGGTCTCCCCGGCCGTCCTCGGGGGTCT 241 185060 CGANTTTCGGCAGGGCTTGCCCGGGGGGTCTTCGGCGGGTCTTGGGGGTCTTGGGGGTCTTGGGGGTCTTGGGGGTCTTGGGGGTCTTGGGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGTCTGGTCGGTCTGGTCTGGGTCTGGTCGGTGTGTGTGTGGTCTGGTGG	
RESULT 15 A48326 LOCUS A48326 VERSION A48326 VERSION A48326 VERSION CORGANISM Streptomyces pristinaespiralis Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomychaeae; Streptomyces. REFERENCE AUTHORS Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F., Crouzet, J., Barriere, J., Debussche, L., Famechon, A., Paris, J. and Dutruc-Rosset, G. STREPTOGRAMINES AND METHOD FOR PREPARING SAME BY MUTASYNTHESIS Patent: WO 9601901-A 4 25-JAN-1996; RHONE POULENC RORER SA (FR)	De 18572 TOTALICANOMICAL PARAMETRA DE CAMALOGICA PROPERTIES DE 18572 TOTATOCCOCOGOGOACCARGAGO CONCOCOGOGOACCA 1281 18512 CONCOTOCOGOGOACCA 1281 186132 CONCOTOCOGOACCA 1281 186131 186132 CONCOTOCOGOACCA 1281 1861 1861 1861 1861 1861 1861 1861	185914GCTGCCGCCCCGGCCCAGCTCACCGTCCGGGATGACCGCGACAGCTACCTGGACA

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Aat58258 Streptomy
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Abd1484 Propionib
Ac64644 Propionib
Ac642465 Prokaryot
Abd14809 Pseudomon
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Claim 11; Page 54-59; 83pp; Japanese

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Transformant producing secondary metabolite modified with functional PT group e.g. benzene with nitrogen-containing substituent at para-posit PT PF1022, with ease at low cost, for application in pharmaceuticals and PT agrochemicals.	DR WPI; 2001-290517/30. DR P-PSDB; AAB82071.	PI Yanai K, Okakura K, Yasuda S, Watanabe M, Miyamoto K, Midoh PI Murakami T;	PA (MEIJ) MEIJI SEIKA KAISHA LTD.	PR 29-SEP-1999; 99JP-00276314.	PF 29-SEP-2000; 2000WO-JP006783. XX	PD 05-APR-2001.	PN W0200123542-A1.	FH Key Location/Qualifiers FT CDS 12061 FT CDS /*tag= a FT /product= "4-amino-4-deoxychorismic acid synthase Yy /product= "4-amino-4-deoxychorismic acid synthase	OS Streptomyces venezuelae.	KW Metabolite; benzene; chorismic acid; p-aminophenylpyruvic acid; KW 4-amino-4-deoxychorismic acid synthase; enzyme; papA; ds. XX	4-amino-4-deoxychorismic acid synthase, papA, coding sequence.	DT 22-JUN-2001 (first entry) .	AC AAF86409;	RESULT 1 AAF86409 ID AAF86409 standard; DNA; 2061 BP. XX	ALIGNMENTS	2 102:3 0.2 110000 3 MIL23006 17	44 184 8.9 110000 11 ADM27081 04	42 189.6 9.2 2190 12 ADV03493 AGC03493	1 189.6 9.2 2190 10 AAD50708 Aad50708	0 190.4 9.2 1323 8 ACA31740 Aca31740	9 192.8 9.4 349980 6 ABO81845 Aborrantor	7 197.8 9.6 1506 11 ABD02207 Abd02207	6 198.2 9.6 1353 8 ACA36033 Aca36033 1	4 210.2 10.2 2160 12 ADO05501 5 201.2 9.8 2199 12 ADO05540	3 210.2 10.2 2160 12 ADO05544	1 210.2 10.2 2160 10 2 210.2 10.2 2160 12	0 210.2 10.2 2160 10 AAD50710 Add5071 Add5071	8 219 10.6 110000 10 ACF67367_49 Continu	6 220.4 10.7 1257 8 ACA45986 Aca45986 7 219 10.6 2019 10 ACF71773 Acf7177	4 231.6 11.2 1338 8 ACA44234 ACA44234 ACA29955 Aca29955	22 234.0 11.4 42000 3 AAA63348 Aaa63348 Aaa63348	21 260 12.6 816 11 ABD15339 Abd15339 Abd3149 Aaa63349	
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                                                                                                                                   The present invention relates to transformants capable of producing PF1022 substance derivatives. These were obtained by transferring a participating in the biosynthesis pathway from chorismic acid to paminophenylpyruvic acid (biosynthesis gene) into a phenylalanine-requiring host derived from an organism producing the PF1022 substant The transformants are producing PF1022 substance derivatives by fermentation, for use as pharmaceuticals or veterinary drugs. The presentation is a substance PF1022 coding sequence from Streptomyces
                                                                                                                                                                                                                                                                                                                                                      Claim
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Example 4; Page 127-128; 188pp; English

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DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; TyyrRS; orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acety/ltransferase; dihydrofolate reductase; dibydrofolate reductase; dibosynthesis; p-aminophenylalanine; pAF; chorismate.
                                                                                                                                                         Composition useful for producing protein comprising unnatural amino has translation system comprising orthogonal tRNA and orthogonal aminoacyl tRNA synthetase.
                                                                                                                                                                                                                                               19-APR-2001;
06-FEB-2002;
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The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-ENA) and an orthogonal aninoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-ENA with at least one unnatural amino acid in the translation system and the O-ENA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Asp12TAG mutant of chloramphenical acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is provided exogenously. The translation system is a cell and the unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid containing the individual genes papABC that encode the translation of chorismate to the unnatural amino acid p-aminophenylalanine (pAF)

Sequence 3305 BP; 445 A; 1327 C; 1121 G; 412 T; 0 U; 0 Other;

Query Match

Local

86.1%; 92.8%;

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DB 8;

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                    CGGGACTTCGGAATCAGCCGCCGGCGGCGATCACCGACAGCGGCCTGCCCGTCCTCGGCGTC
                                                              CCCCTCGAGGACTTCGACGCGATCGTCGTCTCCCCGGGCCCCGGCAGCCCGACCGGGAA
                                                                                    CCCGTCGAGGACTTCGACGCGATCGTCGTGTCCCCGGGCCCCGGCAGCCCCGACCGGGAA
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 CGGGACTTCGGGATCAGCCGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCGGCGTC
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Pred. No. 4.5e-
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RESULT 3 ABZ69799 ID ABZ6

ABZ69799

standard;

DNA;

3305 ВP

1261 CGCATCGACGAGTGCCTCAAGGAGATCCGCAACCGCGAGTCCTACGAGATCTGCCTGJ	1201 GCGGCGGCCTGGCCCCCTGGCCCGCGCGCGCGCACAAAGGACGCCTACCTCZ	1141 GGCCTGGCCGTCCGCGCCCCGGCCGAGCCGCCCCGCCATGGTCTTCCGGATCCCCCCCC	1081 CGCCGGGGCCACGACGACGACGGCGCCGCGCCTGGCTGCGGGAGACGGCCGAGACCCTCJ	1021 GCCGACCGCGCCATCGCCCTCGACCACCAGGAAGGCTGCTGCTGCTGCTGGCTG	961 GCGGAGACCACCGGCGACCCCGCACCCCGCACCCCGACGCCGC	901 CCCGAACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCGGCTACGAGCTGJ 	841 CGGCGCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCGACGGGTCCCCGTCC	781 TACCGCGTCGCCGACGGCGTCCTCCGTCCGCGGCTCCGACGGCACCACGACCGGGI	721 GGCGCCTCGCGCTTCTCCTTCCTCGGCGACGACCGCCGGCCCGCTCGCCGAGTACCTCJ	661 CGCGGCTGCCTGCCCGGCGAGGGCACCACGTTCTGGCTGG	601 TCCCCGTACGAACTCCACGTGCGCCGCGTCGACGTGCTGCCGGACGCCGAAGAGGTAC	541 ATGGCCAACTTCCGCGACCTCGCCCTCGCCCACCGGGCACGGGGCCCACGGGGCCCACGGGGCCCACGGGGCCCACGGGCCACGGGCCCACGGCCACGGCCCACGGCCACGGGCACGCGACGCACGCGACGCACGCGACGCACGCGACGCGACGCACGCGACGCACGCGACGCACGCACGACG	81 CCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCGGCCGGGAACCTTCGGCCGGGAGTCCATCGGCAGCGACTTCGGCCGGGAGTCCATCGGCAGCGACTTCGGCCGGGAGTCCATCGGCAGCGACTTCGGCCGGAGAGTCCATCGGCAGCGACTTCGGCCGGAGAGTCGAGCGACTTCGGCCGGAGAGTCGATCGGCAGCGACTTCGGCCGGAGAGTCGACTGGCCGGAGTCGAGCGAG	421 CTCGAACCCCTCGCCTGGAGCGACGACGGGGTCGTCATGGGCCTGCGGCACCGCGAG	361 CCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTGGCCGCCACCGACCTCCCCGACC	301 CCCATGCACGGCCGGGTCTCCGAGGTGCGGCAACACCGGCGAGGACGTCTTCCGGGGGC	cggcg
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GCAGTGGCGGCGCCCGATGA 2010
                                          GAGGAGTTCAGGCAGACCGTGGTCAAGGCCCGCGCCATGGTCACCGCCCTCGACGGCAGC
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RESULT 4
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DT Plas
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XX DHFR
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KW ORTH
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XX Synt DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; TyrRS; orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase; ds; biosynthesis; p-aminophenylalanine; pAF. Synthetic Plasmid plasc-papabc. 08-APR-2003 WO200285923-A2 ABZ69798; ABZ69798 standard; (first DNA; entry) 12391 ВP

plasmid;

31-OCT-2002

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Best Local Similarity
Matches 1912; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-tRNA with at least one unnatural amino acid in the translation system and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the AsplZTAG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid for use in the biosynthesis of p-aminophenylalanine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The paph gene of S.pristinaespiralis is involved in the biosynthesis of 4 CC -dimethylamino-L-phenylalanine (DMPAPA), a precursor for pristinamycin CI A. Upstream of the paph gene, on the complementary strand, is the snbh CC gene coding for 3-hydroxypicolinic acid-AMP ligase. The region between these two genes was sequenced and two open reading frames were identified. The first (piph) decodes to an amino acid sequence with the bomology to ornithine cyclodeaminase from Agrobacterium tumefaciens. The CC homology to ornithine cyclodeaminase from Agrobacterium tumefaciens. The CC leading to product is likely to catalyse the cyclo-deamination of lysine, leading to production of pipecolic acid. Mutations in the piph gene were shown to affect pipecolic acid synthesis but not the synthesis of 3-cc hydroxypicolinic acid. The second open reading frame (snbf) could be decoded to give a product with homology to hydroxylases of the cytochrome CC decoded to give a product with homology to hydroxylases of the cytochrome CC strains of S.pristinaespiralis which are unable to produce the antiblotic pristinaespiralis which are unable to produce the articles and the pristinaespiralis which are
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RESULT 6
AAT59268
ID AAT5
XX

AAT59268

standard;

CDNA;

2888

ВP

Best Local Similarity

17.7%; 74.2%;

Score 365.4; Pred. No. 3.1

3.1e-38;

Length 2888;

Query Match

Sequence

2888

BP;

390 A; 1319 C; 897 G; 282

U; 0 Other;

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pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papc) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The Papc gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DMPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is likely to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-deoxy 4-aminoprephenate. Disruption of the papB and papc genes can be used to produce strains of S.pristinamycin I but which are unable to produce the antibiotic pristinamycin I but which may be able to produce new, modified forms of it
                                                                                                                                                                                                           biosynthesis of 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptogramin B; antibiotic; biosynthesis; pristinamycin; virginiamy DMPAPA precursor; 4-dimethylamino-L-phenylalanine; papA; papB; papB; papC; isomerisation; aromatisation; N-methyltransferase; ds.
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                                                                                                                                                                                                                                                          Example 1; Page 102-104; 146pp; French.
                                                                                                                                                                                                                                                                                       biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                 Blanc V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUL-1995;
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                                                                                                                                                                                                                 pM genes of S.pristinaespiralis are involved in the 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94FR-00008478
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open reading frame"
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/note= "N-terminal
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/product= "PapB"
2259. .2888
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Paris J, Dutruc-Rosset
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(CIRA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a novel Albicidin family of antibiotics produced by the expression of biosynthetic gene clusters from Xanthomonas albilineans designated as XALB1, XALB2 and XALB3 (albicidin biosynthetic gene clusters 1, 2 and 3). The invention discloses the polynucleotide sequences of these gene clusters, and the proteins encoded by the open reading frames (ORFs) within the gene clusters. Also disclosed are methods for producing an antibiotic and protecting a plant against damage from albicidin and against phytotoxic damage. The present sequence represents an ORF from the Xanthomonas albilineans XALB1 gene cluster.
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                                             The present invention relates to a novel Albicidin family of antibiotics produced by the expression of biosynthetic gene clusters from Xanthomonas albilineans designated as XALB1, XALB2 and XALB3 (albicidin biosynthetic gene clusters 1, 2 and 3). The invention discloses the polynucleotide sequences of these gene clusters, and the proteins encoded by the open reading frames (ORFs) within the gene clusters. Also disclosed are methods for producing an antibiotic and protecting a plant against damage from albicidin and against phytotoxic damage. The present sequence represents Xanthomonas albilineans XALB1 gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                             New transformed host cell, useful for polyketide antibiotics for protecting
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989 GGTCCCCGCACCCCGACGCCGCGTTCCTCTTCGCCGACCGCGCGCG	929 GCTACGTCGGCTACCTCGGCTACGAGCTGAAGGCGGAGACCACCGGCGGACCCCGCGCGCACC 988	870 -GCAGCTCGAACGCCGACGGGTCCCCCGTCGCCCCCGAACTGCCCCTTCGAGTTCAACCTCG 928	821 ACGGCACCACGACCCGGACGCGCCCCTTCTTCAACTACCTGGAGGA 869	761 CGCTCGCCGAGTACCTCACCGTACCGCTCGCCGACGGCGTCGCCGTCCGCCGCCGCCCCG 820	707 GCTCCGTCCTCGAAGGCGCCTCGCGCCTTCTCCTTCCTCGGGCACGACCGCGGCC 760	650 AAGAGGTACGCCGCGGCTGCCTGCCCGGCGAGGGCACCACGTTCTGGCTGG	590 ACGGGGCCGACTCCCCCGTACGAACTCCACGTGCGCCGCTCGACGTGCTGCCGGACGCCC 649	530 GCCGGGAGATCATGGCCAACTTCCGCGACCTCGCCCACCACCACCGGCACCGGCGCC 589	470 ACCGCGAGAAGCCGCTGTGGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCG 529	410 TCCCCGACGAGCTCGAACCCCTCGCCTGGAGCGACGACGGGGTCGTCATGGGCCTGCGGC 469	356 GCCTCCCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTGGCCGCCACCGACC 409	296 CGGAACCCATGCACGGCCGGGTCTCCGAGGTGCGGCACACCGGCGAGGACGTCTTCCGGG 355	236 GCGTCTGCCTCGGCCACCAGGGCATCGCCCAGCTCTTCGGCGGAACCGTCGGCCC 295	176 GGAACGGACTTCGGAATCAGCCGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCG 235	117 -GCTGCCGTCGAGGACTTCGACGGCGATCGTCGTGTCCCCGGGCCCCGGCACCCCACC 175	62 GCGAGGCCACCGGGCAACCCCCCGTCGTCGTGCCCAACGACGCCGACTGGTCGCG 116	2 TGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGTACATCG 61	Best Local Similarity 51.4%; Pred. No. 4.8e-38; Matches 1057; Conservative 0; Mismatches 932; Indels 66; Gaps
	229	69	09	149	889	22 9	369	509	149	389	.5329	269	209	235 15149	5 5	6	969	7;
RESULT AAS5953	B &) B &	D CY	Db Qy	D Q) B Q	DЬ) p (3	;	O D CY) B &	D 5	QD QV	Db Qy	D 5) B 8	D 5	OV.: DB
35	2009 CCCGCGCATGGTCA 2023 		ACCICAGCAICGICAICGCACCATCGIGCIGGCGGACGGCGAGGTCGGCGGCGGCGGGGGGAGTTCGGCGGCGCGCGGCGGGGAAATACGTTTCGGCGCCGCGCGCG	AAGGCCCCCGGGGCGCTTACTCCGGGGCGCTCGAATGGTTCGCCCTCAGCGGCGCCGCCG		TOCGGGGACGCCTGCGGCACCACCACCACCCCCTGCCTGCCGTACGCGCCGCCTTTCCCCCG		TGATGATCGTCGACTTGATGCGCAACGACCTCAACGGCTCGCCGGCAGCGTCA TGATGATCGTCGACTTGATGCGCAACGACCTAAGCCGCGTGGCGGTGCCCGGCAGCGTCA	AGAGGACGAGCGGCCGACCTGGCCGGAGGAGAGACCGGCCGAGAACCC	CGACGGCGGGTCGAGTCCAAGCCATCAAGGGAACCCGCCCG	TICGAGITICCCCGAACTIGTICGTICCTGAGGGCCTCCCCGAGGGGTTCCTCACGATCGATCGAT	ATCCATTGATGCCTACATGCGGGCGAGGGAACCCAGGCGCGTTCGGGGCCTATT	CAACGGCGAGTCGTACGAGATCTGCCTGAGCAACATGGTCACCGCGCGCG	1229 GCGCGCCACGACAAGGACTACCTCAAGCGCATCGACGAGTGCCTCAAGGAGAATCC 1288	TIGCATITICGCTAGGCCTGCGCAGCCGGCTCGGCCCCTGGCCC TIGCATITICGCTAGGCCTGCGCAGCATGGAAATCGAGGTCAATCATGGTCGTC	CTGGCTGCGGAGACCGCCCAGCCGAGCCAGACCGTAGCCGTCCGCCCCAGCCCAGCCAG	CCACTGAGGAGGTATGGTTGCTGGCGCTCGCCGATACGGAGGATCTGTCGGC	15930 CCAATGCCATCCCCGATGCGTTGTGGATGCĢCGTGGAGCGCTTCGTTGCCTTCGACCACG 15989

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Best Local :
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                                                                                                                                                                                                                                   particularly involved in the inflammatory lesions associated with acme vulgaris. A method for detecting the presence or absence of P. acmes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acmes proteins. These antibodies can be used to downregulate expression and activity of P. acmes polypeptides and therefore treat P. acmes infections. The antibodies may also be used as diagnostic agents for determining P. acmes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU46704-AAU46985 and AAU47509. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved infections of bone, joints and the central nervous system, however it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAS59806-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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                                                                CTGCTGGTTGACAACCACGATTCCTTCACCTTCAACCTGGCACACCTATTGGCCGAAGTC
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Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; ds.
                                                        Propionibacterium acnes DNA contig sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733) CC encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to CC polypeptides encompasses expression vectors and host cells comprising a CC polynucleotide of the invention; antibodies against polypeptides of the invention; a comprising a polypeptide of the invention; a complete that expression vectors and host cells comprising a polypeptide of the invention; a complete that expression in the polypeptides, antibodies, fusion proteins, or cell populations, or confident; and a method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, or cell populations, or contient; and a method for inhibiting the presence of P. acnes in a compation. The p. acnes polypeptides, polynucleotides, antibodies, fusion conteins, or cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes concein a completion of an immune response specific for a P. acnes concein and the kit is useful for performing a diagnostic assay. The present cell and the kit is useful for performing a diagnostic assay. The present cell in the invention. Note: The sequence data for this patent did not form to concein the invention. Note: The sequence data for this patent did not form to concein the invention of a figure of the printed specification, but was obtained in electronic format cell and the kit is useful for interesting acne, concein the printed specification, but was obtained in electronic format cell and the content of the printed specification, but was obtained in electronic format cell and the content of the printed specification, but was obtained in electronic format cell cell and the content of the content of the content of the content o
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Zhang Y, Wa
Barth B, Va
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                                                    CGATTGGCTGATGGCGAATTCGACCACGTGGTTATCGGTCCAGGACCTGGCTCCCCGCAC
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Vallieve-Douglass
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ng S, Jen S,
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                                                                                                                                                                                                                                                                                                                                                                                                                     7885 G; 4699 T; 0 U; 6 Other
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Benson DR,
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Jones R, Carter
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ACA42265 standard; DNA; 1362 ВP

19-JUN-2003 (first entry)

Prokaryotic essential gene #23922

Antisense; ds; prokaryotic essential gene; cell proliferation;

Pseudomonas aeruginosa

03-OCT-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                 the 6213 antisense sequences given in the specification where expression (C) of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway (c) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (c) required for proliferation, or that inhibits cellular proliferation; (8) (8) identifying a gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the extent of which each of the strains in present in a culture or collection of contiferation of an organism. The antisense nucleic acids required for cellular proliferation to solate candidate molecules for rational cord and second and content of acids and content or solates candidate molecules for rational cord and content or collection of solate candidate molecules acids are useful.
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published
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Best Local Similarity
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                                                 of Pseudomonas species using biochip technology. Sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD1397-ABD17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-p. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences.
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                                                                                                                                                                                                                                                                                    GGTCCGGGTGCTGCAAACCCTGGAAGGGATGGCCGGGACAGCGTCCC
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                                              otitidis; antigenic protein; immunog; Gram-positive bacterium; infection;
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GAACGGGACTTCGGAATCAGCCGCCGGGCGATCACCGACAGCGGCCTGCCCGTCCTCGGC CTATTGGATCTCGACTTTGATAATGTCATTATTTCACCGGGGCCCGGTAGTCCGGACCGG CCCGTCGA---GGACTTCGACGCGATCGTCGTGTCCCCGGGGCCCCGGCAGCCGGACCGG

FCGGCTTGTGCCGGCAAGTAATTGAAAAGCTTGACAAGCCTATCTTTGGC

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egoga, egoca, eg ATGAAGTCACTCATTATCGATAACTATGATTCTTATACTTACAACTTATACCAGCTTATT ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCACAACCTGTTCCAGTACATC

GGGAAGGTCACAGGGAAAGAGCCCATGGTGATAAAAAATGACCAGATGACCTACCAAGAA

141

81

Query Match Best Local 9

Similarity

13.0%; 48.8%;

Score 267.2; DE Pred. No. 9.6e-20; Mismatches 9

DB 1-26;

963; 9,

Indels Length 2046;

84;

Gaps

Conservative

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CC an isolated polypoptide that is encoded by the polynucleotide (1); (2) an C expression vector comprising the novel isolated polynucleotide (1); its CC complement, degenerate variant or fragment; (3) a genetically engineered CC complement, transferted, transformed or infected with the vector of (2); (6) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological composition vector; (6) a pharmaceutical composition comprising the complement, biological compression vector; (6) a pharmaceutical composition comprising the polypeptides of (1), their biological equivalent or fragment; (8) immunising against Alloiococcus otitidis by administering to a host the cimmunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, (6) or the antibody of (4); and (11) producing a polypeptide by culturing the polypeptides of the culture. (7) can be used from the culture. (7) can be used for treating and diagnosing diseases, drug contidies, polypeptides, antibodies and compositions of the present contidies. The present sequence encodes an Alloiococcus otitidis antigen from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
Sequence 2046 BP;
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18-NOV-2002; 2002US-0426742P
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597 A; 470 C; 493 G;
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                               TGCCTGACCAACATGGTCACCGCGCCGACCGAGGCGACGGCCCTGCCGCTCTACTCCGCG
                                                                                          TATATCAAAGACATTGAAACCATCCAAGACCTGATCAAGGCTGGGGAAAGTTATGAAGTT
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GATCCTGAAGAAGAGTTTGATGAAGTTGTTTTAAAAAGCTAAGGGGGGCCTTGTCCGCCTTG
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                                                                                                                                                                 CC Alloicoccus otitidis genemic DNA, which encodes an antigenic protein.
CC Alloicoccus otitidis is a Gram-positive bacterium. Also described: (1)
CC an isolated polypeptide that is encoded by the polymucleotide (1); (2) an isolated polypeptide that is encoded by the polymucleotide (1); (2) an isolated polypeptide that is encoded by the polymucleotide (1); its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (2) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polypeptide that is comprised in the CC expression vector; (6) a pharmaceutical composition comprising the composition comprising the polypeptide of (1), their biological equivalent or fragment; (8) of the polypeptides of (1), their biological equivalent or fragment; (8) immunising against Alloicoccus otitidis by administering to a host the containing the novel polymucleotide, its degenerate variant or fragment; (8) of the antibody of (4); and (11) producing a polypeptide by culturing the containing the novel polymucleotide, its degenerate variant or fragment; (7) appetide from the culture. (1) can be used in gene therapy. The colympeptide from the culture. (1) can be used in gene therapy. The colympeptide from the culture of can be used in gene therapy. The colympeptide for treating and diagnositions of the present contitions. The present seguence repressing and detecting Alloicoccus otitidis. The present seguence repressing and detecting Alloicoccus cotitidis. The present seguence represents the entire genome of cotitidis, which is given in the exemplification of the
                                                                                                         Query Match
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Matches 999
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                                                                                                                                                                Sequence
                                                                                                                                                                                             present invention
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18-NOV-2002; 2002US-0426742P
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US-09-987-614A-14

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Sequence 14, Application US/09987614A

Patent No. 6833382

GENERAL INFORMATION:
APPLICANT: BLANC, Veronique
APPLICANT: BAMAS-JACQUES, Nathalie
APPLICANT: BAMAS-JACQUES, Nathalie
APPLICANT: BARAS-JACQUES, Nathalie
APPLICANT: BARAS-JACQUES, Nathalie
APPLICANT: BARRIERE, Joen-Claude
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: PAMEIS, Jean-Claude
APPLICANT: PAMEIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A

For

Preparing

Same By

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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,90
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 2220
TYPE: DNA
ORGANISM: Streptomyces pristinaespira
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CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Matches 899; Conserv
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Best Local
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRIC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And
TITLE OF INVENTION: Mutasynthesis
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APPLICANT: THIBAUT, Denis
APPLICANT: BAMAS-JACQUES, Nathalie
APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
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TYPE: DNA
ORGANISM: Streptomyces
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DEBUSSCHE, Laurent
FAMECHON, Alain
PARIS, Jean-Marc
DUTRUC-ROSSET, Gilles
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Pred. No. 4.2e-67;
0; Mismatches 495;
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 4496
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
US-09-987-614A-6
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APPLICANT: BLANC, Ve.
APPLICANT: TILBAUT,
APPLICANT: BLANS-JAC
APPLICANT: BLANCHE,
APPLICANT: COUZET,
APPLICANT: BARRIERE,
APPLICANT: DEBUSSCHI
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US-09-987-614A-6
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Matches 899; Conserv
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DEBUSSCHE, Laurent
FAMECHON, Alain
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BAMAS-JACQUES, Nathalie
BLANCHE, Francis
COUZET, Joel
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Pred. No. 4.2e-67;
0; Mismatches 495,
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            ; Sequence 1, Application US/08765907A
patent No. 6352839
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BLANG-JACQUES, Nathalie
; APPLICANT: BLANCHE, Francis
                                                                                                                                  RESULT 5
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FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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Sequence 1, Application Patent No. 6833382
GENERAL INFORMATION:
APPLICANT: BLANC, Veron
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Best Local Similarity
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APPLICANT: THIBAUT, Denis
APPLICANT: BAWAS-JACQUES, Nathalie
APPLICANT: BLANCHE, Francis
APPLICANT: BLANCHE, Francis
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For
TITLE OF INVENTION: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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; LOCATION: 61.645
; OTHER INFORMATION:
US-08-403-852D-9
                                                                                                                             Query Match
Best Local Similarity 68.7
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION UNMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
PRIOR APPLICATION NUMBER: PS2/11441
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEBLONGENCE/TOCKET NUMBER: 03806.0054-00000
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GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
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STREET: 1300 I Str
CITY: Washington
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62 GCGAGGCCACCGGGCAACCCCCCGTCGTCGTCGCCCAACGACGACTGGTCGCGGCTGC 121
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                                                             TGCGAACCCTGCTGATCGACAACTACGACTCGTTCCACCTACAACCTCTTCCAGATGCTGG
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                                                                                                                                           Score 272.2; DB 2;
Pred. No. 2.2e-36;
0; Mismatches 173;
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122 CCGTCGAGGACTTCGACAGATCGTCATCACCACACCTCGCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCACCTCGCCCACCTCGCCCACCCCCCCC	JULT 8 98-510-646B-9 98-510-646B-9 SENERAL INFORMATION: APPLICANT: Blanch, Veronique APPLICANT: Blanche, Francis APPLICANT: Jacques, Nathalie APPLICANT: Lacroix, Patricia APPLICANT: Lacroix, Patricia APPLICANT: Debussche, Laurent APPLICANT: Debussche, Laurent APPLICANT: Debussche, Laurent APPLICANT: De Crecy-Lagard, Valerie TITLE OF INVENTION: Polypeptides Involved In The TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide Se TITLE OF INVENTION: Coding For These Polypeptides And Their Use NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 2005-3315 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/510,646B FILING DATE: 03-AUG-1995 PRIOR APPLICATION MATA: APPLICATION NUMBER: US 08/403,852 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/403,852	RESULT 8 US-08-510-6 Sequence Patent No GAPPLIO APPLIO APP
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Best Local 9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEPAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODELCE N
HYPOTHETICAL: N
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NAME/KEY:
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ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: S.pristinaespiralis
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US-09-231-818-9
                                                                                                    US-09-231-818-9
                                    Query Match
Best Local S
Matches 392
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Patent No. 6171846
                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR EGO ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FI
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92,
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APPLICANT:
APPLICANT:
                                                                                                                                                                ORGANISM: S.pristinaespiralis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,810
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                  NAME/KEY: CDS
LOCATION: 61.645
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                             STRANDEDNESS:
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STREET: 13
                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                      392;
      N
                                                    Similarity
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T: De Crecy-Lagard, Valerie
INVENTION: Polypeptides Involved In The
INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
INVENTION: Coding For These Polypeptides And Their Use
TGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCCACAACCTGTTCCAGTACATCG
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                                                                                                                                                                                                                                                                                                              645 base pairs
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Zagorec, Monique
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Crouzet, Joel
                                      Conservative
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68.7%;
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                                                                                                                  /product= "gene papA"
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                                    Score 272.2; DB 3
Pred. No. 2.2e-36;
0; Mismatches 173
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                                      173;
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                                      Indels
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TGCGAACCCTGCTGATCGACAACTACGACTCGTTCACCTACAACCTCTTCCAGATGCTGG

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RESULT 10
US-09-635-359B-9
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Patent No. 6670157
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,359B
FILING DATE: 09-Aug-2000
PRIOR APPLICATION NUMBER: US 09/231,818
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Ho
STREET: 1300 I Street,
CITY: Washington
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
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                                                                                                                                                                                                    STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                     Debussche, Laurent
De Crecy-Lagard, Valerie
INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins,
Coding For These Polypeptides A
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Lacroix, Patricia
Thibaut, Denis
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Crouzet, Joel
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                                                                                           Version
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                                                                                           #1.30
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                                                                                                                                                                                                                                                                                                                                             Nucleotide Sequences
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-635-359B-9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                     551
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536 AGATCATGGCCAACTTCCGCGACCTCGCCCT
                                                                                                          491
                                                                                                                                        416 ACGAGCTCGAACCCCTCGCCTGGAGCGACGACGGGTCGTCATGGGCCTGCGGCACCGCG
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LOCATION:
                                 ACCTGCCCCGCTTCGGCGTGCAGTTCCACCCCGAATCGATCAGCAGCGAACACGGCCACC
                                                                                                       CCGACCTGCGCGCCACCCCCACACCGCCGACGGCAGCTGATGGCCGTCGCCCACCGCC
                                                                                                                                                                              ACATCCCCTCCCCGCTGACCGTCGCTCCGCTACCACTCGCTGACCGTCCGGCAACTGCCCG
                                                                                                                                                                                                   GCCTCCCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCCTGGCCGCCACCGACCTCCCCG
                                                                                                                                                                                                                                                   CCGAACCCTTTCACGGCCGCACCAGCGACATCCGCCACGACGGCCAGGGCCTGTTCGCGA
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                                                                   AGAAGCCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCGGCCGGG
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STRANDEDNESS: double
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FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
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Pred. No. 2.2e
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13413
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US-09-252-991A-13413
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                        GGAAGGCCCCCGGGGGCGTCTACTCCGGGGGCGCCCCCGCATGGTTCGCCCTCAGCGGCGCCGC
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13733
LENGTH: 1431
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Marc J. R
TITLE OF INVENTION:
TITLE OF INVENTION:
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Patent No. 6551795
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Best Local Similarity
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Pred. No. 9.2e-36;
0; Mismatches 341
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US-09-252-991A-13943
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Patent NO. 6551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13943
LENGTH: 816
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Best Local Similarity
Matches 435; Conserv
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ORGANISM: Pseudomonas
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                                                                          TGATGATCGTCGACCTGCTGCGCAACGACATCGGACGTTGCCAACCTGGCAGCGTAC
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
ITILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
VMMBER OF SEQ ID NOS: 16825
SEQ ID NO 5760
LENGTH: 1473
TYPE: DNA
ORGANISM: Myxococcus xanthus
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US-09-902-540-5760
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Best Local Similarity
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                                   AGCCCTCGGTGCCGGACCGGCACCCCAGCGACATCTCCTTCCCGGACTCGGAATGGCTGG
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Ger
FILE REFERENCE: 38-10 (15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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Copyright (c) 1993 - 2005 Compugen Ltd.
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N	1773.8	86.1	3305	14	US-10-126-927-68	Sequence 68, Appl
ω	1772.2	86.0	12391	14	US-10-126-927-67	Sequence 67, Appl
4	769.8	37.4	138203	21	US-10-819-386A-1	Sequence 1, Appli
v	606.2	29.4	2196	15	US-10-156-761-1167	Sequence 1167, Ap
ð	606.2	29.4	9025608	15	US-10-156-761-1	Sequence 1, Appl
7	301.4	14.6	9025608	15	US-10-156-761-1	Sequence 1, Appl:

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US-10-430-011-93 US-10-156-961-6781 US-10-138-927-1 US-10-138-927-84 US-10-138-927-85 US-10-138-927-86 US-10-138-927-86 US-10-138-927-86	US-10-282 122A US-10-282-122A US-10-282-122A US-10-138-927-7 US-10-138-927-7 US-10-430-011-8 US-10-430-011-1 US-10-430-011-1 US-10-430-011-1 US-10-126-761-4 US-10-126-761-4 US-10-126-761-4 US-10-128-927-7 US-10-430-011-7 US-10-430-011-1 US-10-430-011-1 US-10-430-011-1 US-10-430-011-1 US-10-430-011-1 US-10-203-295-3 US-10-203-295-3 US-10-203-295-3	US-10-156-761-6148 US-10-716-803-9 US-10-70-21-22A-30135 US-10-501-282-17 US-10-501-282-6651 US-09-738-626-1111 US-10-494-675-25 US-09-738-626-1 US-10-159-257A-1 US-10-292-198-1
93, 6781 1, A 84, 85, 86, 87,	332 332 338 338 338 338 338 338 338 338	Sequence 6148, Ap Sequence 9, Appli Sequence 30135, A Sequence 17, Appl Sequence 17, Appl Sequence 1111, Ap Sequence 1111, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

ALIGNMENTS

RESULT 1 US-10-472-587-1

Sequence 1, Application US/10472587 Publication No. US20040214274A1 GENERAL INFORMATION:

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; NAME/KEY: CDS
; LOCATION: (1)..(2058)
US-10-472-587-1
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APPLICANT: SUMIDA, Naomi
APPLICANT: WATANABE, Manabu
APPLICANT: WATANABE, Manabu
APPLICANT: WORIYA, Tateuki
APPLICANT: MURAKAMI, Takeshi
TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods fo
TITLE OF INVENTION: Producing The Same And Novel Biosynthesis Genes
TILE REFERENCE: 2003-1302A/MMC/00144
CURRENT APPLICATION NUMBER: US/10/472,587
CURRENT FILING DATE: 2003-9-22
PRIOR APPLICATION NUMBER: 82227/2001
PRIOR APPLICATION UMBER: 82227/2001
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 40
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2061
Query Match
Best Local Similarity
                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces venezuelae FEATURE:
        100.0%;
     Score 2061;
Pred. No. 0;
                                DB 20;
                             Length 2061;
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1021 GCCGACCGCCATCGCCCTCGACCACCAGGAAGGCTGCTGCTACCTGCTGGCCCTCGAC 1080	61 GCGGAGACCACCGGCGACCCGCGCACCGGTCCCCGCACCCCGACGCGCGTTCCTCTC 1	901 CCCGAACTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACGCTCGGCTACGAGCTGAAG 960	1 CGGCGCCCCTTCTTCAACTACCTGGAGGAGCAGCTCGAACGCCCGACGGGTCCCCGTCGCC 9	781 TACCGCGTCGCCGACGGCGTCGTCTCCGTCCGCGGCTCCGACGGACCACGACCCGGACC 840	721 GGCGCCTCGCGCTTCCTCCTCCGGCGACGACGACGGCGCCGCTCGCCGAGTACCTCACC 780	0-0	601 TCCCCGTACGAACTCCACGTGCGCGCGTCGACGTGCTGCCGGACGCCGAAGAGGTACGC 660	541 ATGGCCAACTTCCGCGACCTCGCCCTCGCCCACCACCACGGGCCACGGGCCCACGGGCCCACGGGCCCACGGGCCCACGGGCCCACGACG	481 CCGCTGTGGGGCGTCCAGTTCCACCCGGAGTCCATCGGCAGCGACTTCGGCCGGGAGATC 540	421 CTCGAACCCCTCGCCTGGAGCGACGACGACGGGTCGTCATGGGCCTGCGGCACCGCGAGAAG 480	361 CCCTCGCCGTTCACCGCCGTGCGCTACCACTCCCTGGCCGCCCCCGACCTCCCCGACGAG 420	301 CCCATGCACGGCCGGGTCTCCGAGGTGCGGCGACACCGGCGAGGACGTCTTCCGGGGGCCTC 360	241 TGCCTCGGCCACCAGGGCATCGCCCAGCTCTTCGGCGGAAACCGTCGGCCTCGCCCCGGAA 300	181 CGGGACTTCGGAATCAGCCGCCGGGCGATCACCGACAGCCGGCCTGCCCGTCCTCGGCGTC 240	121 CCCGTCGAGGACTTCGACGCGATCGTCGTCGTCCCCGGGCCCCGGCAGCCCGGGAA 180	61 GGCGAGGCCACCGGGCAACCCCCCGTCGTCGTGCCCAACGACGCCGACTGGTCGCGGCTG 120	1 ATGCGCACGCTTCTGATCGACAACTACGACTTCGTTCACCCACAACCTGTTCCAGTACATC 60	ches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 2 US-10-126-927-68 ; Sequence 68, Application US/10126927	Qy 2041 GCCGTGGCGGGCGCCCGATGA 2061	1981 GAGGAGTTCACCGAGACCGTG 	1921 GCCGACGCCAGGCGGAGTTCGGCGTCGGCGGGGGGATCGTGTCCCTTCCGACCAGGAG	1861 1861	1801 ACCATGGAGATCATCGACGCCTGGAGGAAAGGCCCCGGGGCGTTACTCCGGGGCGCTC	1741 GCGGCTGCGTACGCGCCGCCTTCCCCGGCGGCTCCATGACCGCGCGCCCAAGAAGCGC	1681 GCGCCCGTGCACCAGCTGGTGTCGACCATCCGGGGACGGCTGCGGGCCCGGCACCAGCACC	1621 AACAGCGTCTGCGCATCGGCTCCGCTCCACGTGCCCCGGCTCTTCGAGGTGGAGACCTAC	1561 GGCCGGAGAAGGACCGGGCCGAGAACCTCATGATCGTCGACCTCGCAACGACCTC 1561 GGCCGGAGAAGGACCGGGCCGAGAACCTGATGATCGTCGACCTGGTCCGCAACGACCTC 1561 GGCCGGAGAAGGACCGGGCCGAGAACCTGATGATCGTCGACCTGGTCCGCAACGACCTC	1501 GGGACCCGCCGGGGCGACCGGGGAGGAGGAGGAGCGGCCGACCTGGCC	1441 TCGCCCGAGCGGTTCCTCACGATCGGCGGCGGCGGCGTCGAGGCCCATCAAGCCATCAAGCCCAACAAGCCCAACAAGCCCAACAAGCCCAACAAGCCCAACAA	1381 ATCAGCCCCGTCCCGTACGGCGCCCTGCTCGAGTTCCCCGAACTGTCGGTGCTGAGGGCC 1381 ATCAGCCCCGTACCGCGCCCCTGCTCGAGTTCCCCGAACTGTCGGTGCTGAGCGCC	1321 AACATGGTCACCGCGCCGACCGACGGCCTTACCGCCTTACTCCGCGCTGCGCGCCTGCCGCGCTGCCGCCTTACTCCGCGCTTACTCCGCGCTGCCGCGCCGACGGCCGACGGCCCTTGCCGCTCTACTCCGCGCTGCCGCGCCCGACCGGCCGTGCCGCTCTACTCCGCGCTGCCGCGCCCGCC	1261 CGCATCGACGAGTGCCTCAAGGAGATCCGCACGGGGAGTCGTACGAGATCTGCCTGACC	1201 GUGGUGGUGGUGGUGUGUGUGUGGUGGGGGGGGGGACAAGGACGCTACCTCAAG 1201 GUGGGGGCCGGGTTCGGCCCCTTGGCCCCGCGCGCGCCACGACAAGGACGCCTACCTCAAG	120 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1081 CGCCGGGGCCACGACGACGACGACGCCCGCGCCTGGCGGAGACGGCCGAGACCCCTCACC	OV 1081 CGCCGGGGCCACGACGACGGCGCCCGCGCGTGGCTGGGGGAGACGGCCGAGACCCTCACC 1140

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GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Schultz, Peter G
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Wang, Lei
APPLICANT: Wang, Lei
APPLICANT: Wangerson, John C
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Meggers, Eric L
APPLICANT: Santoro, Stephen W
APPLICANT: Dang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-06
NUMBER OF SEQ ID NOS: 79
SOPTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 3305
TYPE: DNA
ORGANISM: Streptomyces venezuelae
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Query Match Best Local Similarity 92.8%; Pred. No. 0; Matches 1912; Conservative 0; Mismatches 98; Indels 51; Gaps 3; Matches 1912; Conservative 0; Mismatches 98; Indels 51; Gaps 3; Qy 1 ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCACAACCTGTTCCAGTACATC 60 24 ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCAGAACCTGTTCCAGTACATC 83 Qy 61 GGCGAGGCCACCGGGGCAACCCCCCGTCGTCGTCGTCGAACGCGCGACTGGTCGGGGCTG 120	SOFTWARE: Patentin SEQ ID NO 67 LENGTH: 12391 TYPE: DNA ORGANISM: Plasmid S-10-126-927-67	FILE REFERENCE: 54-000120US CURRENT APPLICATION NUMBER: US/10/126,927 CURRENT FILING DATE: 2002-04-19 PRIOR APPLICATION NUMBER: US 60/285,030 PRIOR APPLICATION NUMBER: US 60/355,514 PRIOR APPLICATION NUMBER: US 60/355,514 PRIOR FILING DATE: 2002-02-06	APPLICANT: Anderson, John C APPLICANT: Chin, Jason APPLICANT: Liu, David R APPLICANT: Magliery, Thomas APPLICANT: Meggers, Eric L APPLICANT: Medi, Ryan A APPLICANT: Pastrnak, Miro APPLICANT: Santoro, Stephen W APPLICANT: Santoro, Stephen W	ESULT 3 5-10-126-927-67 Sequence 67, Application US/ Publication No. US2003008257 GENERAL INFORMATION: APPLICANT: The Scripps Rese APPLICANT: Schultz, Peter APPLICANT: Wang, Lei	Qy 1981 GAGGAGTTCACCGAGACCGTGGTAAAGGCCCGCGCCATGGTCACCGCCCTCGACGGCAGC 2040	Db 1810 GGATGGTTCGGCGTCGGCGGCGGCGGCGATCGTCATCCGACCATCGTGCTG 1980 Oy 1921 GCCGACGGCGAGGTTCGGCGTCGGCGGCGGCGATCGTGTCCCCACCAGGAG 1980 Db 1870 GCCGACGGCCGAGGTTCGGCGTCGGCGGGGGGGATCGTGTCCCTCTCCGACCAGGAG 1929	1681 GCGCCGTGCACCAGCTGGTGTTCGACCATCCGGGGACCGGCCCGGCACCACCACCACCACCACCACCAC
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RESULT 4
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Sequence 1, App
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GENERAL INFORMA
APPLICANT: KOR
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; Sequence 1, Application US/10819386A
; Publication No. US20050089884A1
; GENERAL INFORMATION:
APPLICANT: Korea advanced Institute of Scie
APPLICANT: Shanghai Jiaotong University
APPLICANT: LEE, Sang Yup
APPLICANT: LEE, Sang Yup
APPLICANT: DENG, ZIXIN
APPLICANT: JEONG, Kii Jun
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; TITLE OF INVENTION: Genes for the Synthesis of FILE REFERENCE: PO03-B015; CURRENT APPLICATION NUMBER: US/10/819,386A; CURRENT FILING DATE: 2004-04-06; PRIOR APPLICATION NUMBER: KR10-2003-0074035; PRIOR FILING DATE: 2003-10-23; NUMBER OF SEQ ID NOS: 28; SOFTWARE: Patentin version 3.2; SEQ ID NO 10.00; SEQ ID N
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; TYPE: DNA
; ORGANISM: Streptomyces
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; TYPE: DNA
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US-10-156-761-1167
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER DE EGO 1500-08-02
NUMBER DE EGO 1500-08-02
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SEQ ID NO 1167
LENGTH: 2196
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Best Local Similarity 58.3%;
Matches 1262; Conservative
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RESULT 6
US-10-156-761-1/c
US-10-156-761-1/c
Sequence 1, Application US/10156761
Publication No. US20030119018A1
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697

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Best Local Similarity 58.3%;
Matches 1262; Conservative
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NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
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ORGANISM: Streptomyces avermitilis
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                                          1469816 GGATGTACACCGACGCGCCCCGCGCGTTCTGGCTCGACAGCTCCCGGGTCGAGGAGGGAC 1469757
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    CCTCGCGCTTCTCCTTCCTCGGCGACGACGGCCCGCCGCCGAGTACCTCACCTACC
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1802 CCATGGAGATCATCCGCCTGGAGGAAGGCCCCCGGGGCGTCTACTCCGGGGCGCTCG
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-02
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Matches 948; Conservative
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JS 2001-272697
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6148
LENGTH: 1479
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US-10-156-761-6148
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                                                                                                                                                                                                           US-10-156-761-6148
                                                                                     Query Match 13.6%;
Best Local Similarity 51.9%;
Matches 764; Conservative
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1479)
                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces
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Publication No. US20040229236A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Faranteet, N.W., Suite
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM Flo COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                          FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/716,803 FILING DATE: 20-Nov-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                   APPLICATION NUMBER: US 09/635,359
FILING DATE: 09-AUG-2000
APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
        NAME: Arrigo, REGISTRATION
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De Crecy-Lagard, Valerie
INVENTION: Polypeptides Involved in The
Siosynthesis Of Streptogramins,
Coding For These Polypeptides Ar
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Crouzet, Joel
Jacques, Nathalie
Lacroix, Patricia
Thibaut, Denis
Zagorec, Monique
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        Salvatore J.
VUMBER: 46,063
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ite 700
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Sequence 30135, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
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Matches 392;
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TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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LOCATION: 61..645
OTHER INFORMATION: /
SEQUENCE DESCRIPTION: SEQ
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TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 30135
LENGTH: 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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ORGANISM: Pseudomonas
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Malone, (
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Forsyth, R.
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Trawick, John
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Zyskind, Judith
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Haselbeck, Robert
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Pred. No. 1.2e-49;
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APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS)
TITLE OF INVENTION: POLYPETIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS #
FILE REFERENCE: AM100780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
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PRIOR FILING DATE: 2002-11-25
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PRIOR FILING DATE: 2001-11-29
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PRIOR FILING DATE: 2002-11-18
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RESULT 12
US-10-501-282-6651/c
US-10-501-282-6651, Application US/10501282
Sequence 6651, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOICOCCUS OTITID
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FILE REFERENCE: AM100780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR FILING DATE: 2001-11-29
PRIOR PRIOR PRICATION NUMBER: 60/426,742
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 6651
LENGTH: 1754382
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US-09-738-626-1111
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Best Local Similarity
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SEQ ID NO 1111
LENGTH: 1860
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                1059 CAĂAGATGAGTATCTCGACAAAATTCGCAGAGCCCAGGAGCTGATTACTCGCGGCGAATC
                                                                                                                                                                                                                                                                                                                                   1242 САЛОБАСССТАССТСАЛОСССАТСВАСОВСТВССТСАЛОВАСЛОТОВОТОВ 1301
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                                                                                                                                                                                      CTACTCCGCGCTGCGCCCATCAGCCCCGTCCCGTACGGCGCCCTGCTCGAGTTCCCCGA 1421
GGAATCAAAGCCCATTAAAGGCACCAGGCCGCGTGGGCGAACAGCGCGCAAGAAGACCAAGA 1358
                                                                                                                                                 CTATCTAGCACTGCGTGGGGGCCAATCCCCACCGCATATGGTGCGTATCTTCAGCTGGGGGA
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                                    GACCAGGAGGAGTTCACCGAGACCGTGGTAAAGGCCCGCGCCATGGTCACCGCCCTC 2031
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Pred. No. 5.6e-49;
0; Mismatches 312;
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APPLICANT: Colder, Oskar
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Burkhard
APPLICANT: Klopprogge, Corinna
APPLICANT: Klopprogge, Corinna
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: Genes coding for metabolic pathway pro
FILE REFERENCE: BGI-163US
CURRENT PHILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: US/10/494,675
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: DE 101 54 292.1
PRIOR FILING DATE: 2001-11-05
INVENT: DATE: 2001-11-05
SEQ ID NO 25
LENGTH: 2005
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US-10-494-675-25
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                                                        Query Match
Best Local S
Matches 467
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                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: (101
                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum
1242 CAAGGACGCCTACCTCAAGCGCATCGACGAGTGCCTCAAGGAGATCCGCAACGGCGAGTC
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467; Conserv
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                                                                       12.9%;
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                                                   Score 266.8; DB 21; .Pred. No. 5.5e-49; 0; Mismatches 312;
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Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAVASHI, MIKIRO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
      RESULT 15
US-09-738-626-1
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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LENGTH: 3309400
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Best Local Similarity
Matches 467; Conserv
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TYPE: DNA
ORGANISM: Corynebacterium
                                     1053796 TGCTCTGTCTGATCCGGAGGCTGAGTGGGAGGAAATCCGCGTTAAATCACGGCCTCTGCT
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2022 CA 2023
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Pred. No. 1.8e-49;
0; Mismatches 312;
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Search completed: October 5, 2005, 09:56:39

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ALIGNMENTS

VERSION KEYWORDS LOCUS DEFINITION RESULT 1 CA003778 FEATURES REFERENCE COMMENT SOURCE ACCESSION TITLE AUTHORS ORGANISM JOURNAL source Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensetr 3, 06466, Gatersleben, Germany Tel: 039402-5522 Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum. 529 bp HS15114r HS Hordeum vulgare subsp. 5-PRIME, mRNA sequence. CA003778 Email: stein@ipk-gatersleben.de Insert Length: 529 Std Error: 0.00 Plate: 15 row: I column: 14 Unpublished (2002 Contact: Stein Nils Barley ESTs from germinating seeds Zhang, H., Potokina, E., Michalek, W., CA003778.1 GI:24280760 Fax: 039482-5595 (bases 1 to 529) primer: Ml3rev /tissue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="XLI0-Gold"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="Type="color: pBluescript SK+; Site_1: EcoRI (5'-end of DNA); Site_2: XhoI (3'-end of CDNA); Due to a coloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also sub_species="vulgare" db_xref="GABI:258990" /mol_type="mRNA" /cultivar="barke" Location/Qualifiers clone="HS15I14" organism="Hordeum vulgare subsp. vulgare" _xref="taxon:112509" mRNA linear EST 23-OC vulgare cDNA clone HS15I14 Weschke, W., Stein, N. and EST 23-OCT-2002 Tracheophyta;

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Email: cray....
Class: shotgun.
Class: Location/Qualifiers
                                                                                                                                   Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation am Psedomonas aeruginosa library J. Bacteriol. (2002) In press
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msh2 1411.x1 msh Pseudomonas
genomic survey sequence.
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B2570522.1 GI:27205583
                                                                        Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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                                                                                                                            Contact: Chris K.
                                                                                                                                                                                                                       Pseudomonadaceae; Pseudomonas.
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                Tyler, B. Not Published Unpublished (2003)
                                                                                                                Phytophthora sojae
Phytophthora sojae
Eukaryota; stramenopiles;
  Contact:
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                                                                           (bases 1 to 653)
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/strain="WSH"
/db_xref="taxon:287"
/clone="msh2_1411"
/clone_lib="msh"
/note="Environmental isolate. W
Tyler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pseudomonas aeruginosa"
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FORWARD: BK reverse primer
BACKWARD: BK reverse primer
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Seq primer: BK reverse primer
High quality sequence stop: 653
                       GCGGCGCCGGCCGACCTCAGCATCGTCATCCGCACCATCGTGCCTGGCCGAC 1926
                                                                               ACCGCCTGGAGGAAGGCCCCCGGGGCGTCTACTCCCGGGGCGCTCGGATGGTTCGCCCTCA
                                                                                                                                                                                                          TCGGCTCCGTCCACGTGCCCCGGCTCTTCGAGGTGGAGACCTACGCGCCCGTGCACCAGC
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CCGGGTTCCTGGACACGGNCATCGCCATCCGCACCATGGTGGTCAAGGAC
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                                                                                                                                                                                                                                                                                                          GCGCCGAGCACATCATGCTGGTGGACCTGGGCCGCAACGACGTCGGCCGCGTGGCCAAGC
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                                                                                                                      Pratt Dr., Blacksburg, 540-231-7318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="sz8008G04"
/tissue_type="zoospores"
/cell Ine="p6497"
/dev stage="Free swimming"
/dev stage="Free swimming"
/clone lib="USDA-IFAFS.Expression of Phytophthora sojae
/clone during infection and propagation_sz8"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
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/db_xref="taxon:67593"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole-Genome-Sequence variation among Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1043)
Spencer, D.H., Raymond, C.K., Smith, E.E.,
Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: craymond
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 2066857244
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Other_GSSs: OGAAG11TC
Contact: Cathy Whitelaw
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OGAAG11TC ZM_0.7_1.5_KB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
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GCACCATGGAGATCATCGACCGCCTGGAGGAAGGCCCCCGGGGCGTCTACTCCGGGGCGCC 1858
                                                                         CCGCCGCCTGCGTACGCGCCGCCTTCCCCCGGCGGCTCCATGACCGGCGCGCCCAAGAAGC 1798
                                                                                                                        ACAGAAGTGTTCACACCATGGTGAGTACCGTCTGCGGAACAAAGAAGCCCAGATCTAAGCC
                                                                                                                                                 ACGCGCCCGTGCACCAGCTGGTGTCGACCATCCGGGGACGGCTGCGGCCCCGGCACCAGCA 1738
                                                                                                                                                                                             TCGGCAAGGTCTGCGAGCCAGGGAGCGTGCATGTCCCACGCCTCATGGACGTTGAATCAT
                                                                                                                                                                                                                         TCAACAGCGTCTGCGCGATCGGCTCCGCTCCCCGGCTCTTCGAGGTGGAGACCT
                                                                                                                                                                                                                                                                 CCACCAGCGAAAAAGACCAGGCCGAGAACCTGATGATTGTCGACCTCTTAAGAAACGATC
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                                                      CCGTTGATTGTGTGAAAGCGGCCTTTCCAGGCGGTTCGATGACCGGGGCTCCAAAAGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:4577"
/clone="zmMan015004"
/clone_lib="ZM_0.7_1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/mol_type="genomic D
/strain="B73"
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Pred. No. 1.4e-20;
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RESULT 7
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JOURNAL
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Best Local Similarity
Matches 283; Conserv
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ537360.1
GSS.
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OGAGD95TC ZM2 0.7 1.5 KB
genomic survey sequence.
BZ537360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                 CCGGCCGGGAGAAGGACCGGGCCGAGAACCTGATCGTCGACCTGGTCCGCAACGACC
                                                                                                                              TCAACAGCGTCTGCGCGATCGGCTCCACGTGCCCCGGCTCTTCGAGGTGGAGACCT
CCGTTGATTGTGTGAAAGCCGCCCTTTCCAGGCGCTTCGATGACCGGGGCTCCAAAAGTCA
                                                                                ACGCGCCCGTGCACCAGCTGGTGTCGACCATCCGGGACGGCTGCGGCACCAGCA 1738
                                                                                                                                                                 CCACCAGCGAAAAAGACCAGGCCGAGAACCTGATGATTGTCGACCTCTTAAGAAACGATC
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                        ACAGAAGTGTTCACACCATGGTGAGTACCGTCTGCGGAACAAAGAAGCCAGATCTAAGCC
                                                                                                           TCGGCAAGGTCTGCGAGCCAGGGAGCGTGCATGTCCCACGCCTCATGGACGTTGAATCAT
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                                                                                                                                                                                                                                                                                        /clone="ZMMBMa0053P22"
/clone_lib="ZM2_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0."
methylation filtered genomic DNA library"
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                           organism="Zea mays"
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Pred. No. 1.4e-20;
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Query Match
Best Local S
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                                                                                                                                                                                                                                                            283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_GSSs: PUIIR58TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 810)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                              Similarity
                                    ACGCGCCCGTGCACCAGCTGGTGTCGACCATCCGGGGACGGCTGCGGCCCCGGCACCAGCA 1738
                                                                                                               TCAACAGCGTCTGCGCGATCGGCTCCGTCCACGTGCCCCCGGCTCTTCGAGGTGGAGACCT
                                                                                                                                                                     CCACCAGCGAAAAAGACCAGGCCGAGAACCTGATGATTGTCGACCTCTTAAGAAACGATC
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ACAGAAGTGTTCACACCATGGTGAGTACCGTCTGCGGAACAAAGAAGCCAGATCTAAGCC
                                                                                    TCGGCAAGGTCTGCGAGCCAGGGGAGCGTGCATGTCCCACGCCTCATGGACGTTGAATCAT
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                  /clone lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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mol
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/clone="ZMMBTa0592I20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="B73"
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                                                                                                                                                                                                                                                       Score 178; DB 9;
Pred. No. 1.4e-20;
0; Mismatches 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole,R., Fogarty,S., Tang,K., Howe,D.K., Sibley,L.D., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wile,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvili,R., Fedele,M., Belaygorod,L., Franklin,C., Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Richey,J., Waterston, Carr, M., Grow,A., Maguire, M., Wadkins, M., Richey,J., Waterston, Carr, M., Grow, A., Maguire, M., Wadkins, M., Richey, M., Waterston, Carr, M., Waterston, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Sandy Clifton, Ph.D. - Neospora
USDA-WashU Neospora EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Wilson,R.
USDA-WashU Neospora EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact David Sibley (toxoest@borcim.wustl.edu) information relating to organism, libraries, or Seq primer: -40RP from Gibco.
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314 286 1810
                  /dev_stage="Tachyzoite"
//lab host="ElectroTen Blue cells (Stratagene)"
//lab host="ElectroTen Blue cells (Stratagene)"
//clone libb="Nc-LIV Tachyzoite cDNA Library"
//note="Vector: pBluescript II SK+Vector type: plasmid;
Site 1: EcoRI; Site 2: XhoI; The cDNA library was
constructed by Keliang Tang, and Robert Cole at Washington
University. cDNA was synthesized from Poly(A)+ mRNA using
an oligo-d(T) primer containing a XhoI site. Following
second strand synthesis, EcoRI adapters were ligated to
the cDNA, and products were size-selected on sephacryl
S500. The cDNA were directionally cloned into the
EcoRI/XhoI prepared pBluescript II SK+ vector, and
electroporated into ElectroTen Blue cells (Stratagene).
The library may contain a small percentage of host or
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Neospora ca:
/mol_type="mRNA"
/db_xref="taxon:29176"
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haloarcula marismortui ATCC 43049
Haloarcula marismortui ATCC 43049
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                              Institute for Systems Biology
1441 North 34th Street, Seattle,
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                                                                                                                                                                                         Low-pass Sequencing for Microbial Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Goo,Y., Roach,J., Glusman,G., Baliga,N.S., DasSarma,S., Ng,W.V. and Hood,L.
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660 bp DNA linear GSS 30-JUL-2/HM7_0152.x1_059.abl Hm pUC18 Library Haloarcula marismortui ATCC 43049 genomic 5', genomic survey sequence.
                                                                                                                                                                         Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                  Contact: Goo Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halobacteriaceae; Haloarcula.
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                                                                                                                                              shotgun
                                                                                        1. .660
/organism="Haloarcula marismortui ATCC 43049"
/mol_type="genomic DNA"
/strain="ATCC 43049"
                                                                                                             Location/Qualifiers
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Pred. No. 6.4e-20;
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                                                                              EST:
Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
                                                                                                                                                   CO024641
894 bp mRNA linear EST EST803025 Coccidioides posadasii spherule cDNA library, kb Coccidioides posadasii cDNA clone CIFA227 3' end, mRI CO024641
CO024641.1 GI:48551893
EST.
      Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides
spherules via expressed sequence tags
Unpublished (2003)
                                                                     Onygenales; mitosporic Onygenales; 1 (bases 1 to 894)
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/clone lib="Hm pUC18 Library"
/note="Vector: pUC18; Site_1: SmaI; A shotgun library was
constructed from Haloarcular marismortui genomic DNA using
pUC18/SmaI/BAP plasmid"
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Pred. No. 1.6e-19; 
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Contact: Gardner MJ
The Institute for Genomic Re
9712 Medical Center Drive, F
Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: gardner@tigr.org.
Location/Qualifiers
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                                                                            CTGGAGGAAGGCCCC---CGGGGCGTCTACTCCGGGGCGCTCGGATGGTTCGCCCTCAGC
                                                                                                                                                   TTCCCCGGCGCTCCATGACCGGCGCGCCCAAGAAGCGCACCATGGAGATCATCGACCGC
                                                                                                                                                                                      ACAACCATTCAATCCCACATCGCCCCCAACGTCGGCGGCGTCCAGGTTCTCGAGCGATGC
                                                                                                                                                                                                                    TCGACCATCCGGGGACGGCTGCGGCCCGGCCACCAGCACCGCCTGCGTACGCGCCCCCC
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Coccidioides posadasii spherule cDNA library, 0.5
kb "
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/lab_host="E. coli DH10B,
/clone_lib="Coccidioides;
0.5 to_5.3 kb"
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Pred. No. 7.6e-19;
0; Mismatches 387
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Best Local Similarity
Matches 334; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute for Systems Biology
1441 North 34th Street, Seattle,
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Goo Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halobacteriaceae; Natrialba.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natrialba asiatica
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                                                                         GGCTCCGCGCCGACCTGGCCGGCCGGGAGAAGGACCGGGCCGAGAACCTGATGATCGTCG
                                                                                                                                                  TCGAGTCCAAGCCCATCAAGGGGACCCGCCCCCGGGGCGCACCGCGGAGGAGGACGAGC
                                                                                                                                                                                       ACCTGACCGTCGTCGGTGCAAGCCCCGAAACGCTGCTATCGGTGCGCGGGC----GAGAAG
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                                      GACTGGCGGGCGAGATGCTCGCAGACGGGAAGGAGCGCGCCGAACACACCATGCTGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="ATCC 700177"
/db_xref="taxon:64602"
/clone_lib="Na pUC18 Library"
/note="Vector: pUC18; Site_1: SmaI; A shotgun library
constructed from Natrialba asiatica genomic DNA using
pUC18/SmaI/BAP plasmid"
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Pred. No. 9.8e-19;
0; Mismatches 239;
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Best Local Sim
Matches 344;
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Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eu
Eukaryota; mitosporic Onygenales; Coccidioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onygenales; mitosporic Onygenales; Coccidioi 1 (bases 1 to 750)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CO028609 750 bp mRNA linear EST 10-JUN-2004
EST806993 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone CIFAS82 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: EST806994
Contact: Gardner MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: gardner@tigr.org.
Location/Qualifiers
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                                                                         CCTCGCCCGAGCGGTTCCTCACGATCGGCGCCGACGCGGCGTCGAGTCCAAGCCCATCA 1498
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                                                                                                               Conservative
                                                                                                                                                                                                        /note="Vector: pExpress
Coccidioides posadasii s
kb "
                                                                                                                                                                                                                                                            /dev_stage="spherules"
/lab_host="E. coli DH10B,
/clone_lib="Coccidioides
0.5 to 5.3 kb"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Coccidioides
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                        /clone="CIFAS82"
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                                                                                                                           8.0%;
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Pred. No. 2.5e-18;
0; Mismatches 277;
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 818)
1 (bases 1 to 818)
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Contact: Gardner MJ
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                                                                                                                                                                                                                                                         Institute for Genomic 1
2 Medical Center Drive,
301 838 3519
301 838 0208
                                                                                                                                                                                                          gardner@tigr.org.
Location/Qualifiers
                                                                                                                                  /dev_stage="spherules"
/lab_host="E. coli DH10B,
                                                         /db_xref="taxon:199306"
/clone="CIFB368"
                                                                                                          mol_type="mRNA"
strain="C735"
                                                                                                                                                            organism="Coccidioides
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1 (bases 1 to 820)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags
Unpublished (2003)
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                                                                                                                          Coccidioides posadasii
Coccidioides posadasii
Coccidioides posadasii, Pezizomycotina; El
Eukaryota; Fungi, Ascomycota; Pezizomycotina; El
Onygenales; mitosporic Onygenales; Coccidioides
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CO034510 820 bp mRNA linear EST 10-JUN-2004
EST812894 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone CIFBU13 3' end, mRNA sequence.
C0034510.1
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Similarity 55.1%;
44; Conservative
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GI:48571664
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Pred. No. 2.5e-18;
0; Mismatches 277;
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Email: gardner@tigr.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: EST812895
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
                                                                                                                                                              TGCTGGCCGACGGCGAGGTCGGCGTCGGCGGGGGGGGGATCGTGTCCCTCTCCGACC 1975
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                                 GCAGCGCCGTGGCGGGCGCCCGAT 2059
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/lab host="E. coli DH10B, Tl phage resistant"
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/clome_libe="Occidioides posadasii spherule cDNA library,
0.5 to 5.3 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb "
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/clone="CIFBU13"
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Pred. No. 2.5e-18;
0; Mismatches 277;
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Search completed: October

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Job time : 7804.14 secs

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Ggn2 | JUSPT0 gpool h/US10089514/runat_04102005_105744_8033/app_query.fasta_1.1621
-Q=/Ggn2 | JUSPT0 gpool h/US10089514/runat_04102005_105744_8033/app_query.fasta_1.1621
-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGU=200 -THR SCONE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10089514 @CGN 1 1 8782 @runat 0410205_105744_8033 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBILOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOD=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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п	AE006363		102	24.1	859.5	43
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05727 Arabidop	AC00572		1070	25.3	904.5	41
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3189 Clostrid	AP00318	050 1	œ	26.2	937.5	39
51926 Phaeodac	AC151	9	œ	28.8	1029	38
8359 Coryneb	BX24835	ហ	ω		1068.5	37
198356 Sequenc	AR19835	ი	44	30.7	1096.5	36
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ALIGNMENTS

		6			RE	SC	VE	DB 071
		COMMENT	JOURNAL	AUTHORS TITLE	REFERENCE	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	BD178313 LOCUS DEFINITION
PI MURAKAMI PC C12N15/61,C12N1/15,C12P17/14//(C12N1/15,C12R1:645),(C12P17/14,	PN WO 02077244-A/1 PD 03-OCT-2002 PF 03-OCT-2002 PF 22-MAR-2002 WO 2002JP002782 PR 22-MAR-2001 JP 01P 082227 PR 22-MAR-2001 JP 01P 082227 PI KOJI YANAI,NAOMI SUMIDA,MANABU WATANABE,TATSUKI MORIYA,TAKESHI	MEIJI SEIKA KAISHA LTD,KOJI YANAI,NAOMI.SUMIDA,MANABU WATANABE, TATSUKI MORIYA,TAKESHI MURAKAMI OS Streptomyces venezuelae	the same and novel biosynthetic gene Patent: WO 02077244-A 1 03-OCT-2002;	Yanai, K., Sumida, N., Watanabe, M., Moriya, T. and Murakami, T. Transformant producing PF1022 substance and process for producing	Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycinaae, Streptomycetaceae; Streptomyces. 1 (bases 1 to 2061)	WO 02077244-A/1. Streptomyces venezuelae Streptomyces venezuelae	The same and nover prosynthetic gene. BD178313. BD178313.1 GI:30015578	BD178313 2061 bp DNA linear PAT 16-APR-2003 Transformant producing PP1022 substance and process for producing

Qy 241 GlyAlaSerArgPheSerPheLeuGlyAspAspArgGlyProLeuAlaGluTyrLeuThr	Qy 221 ArgGlyCysLeuProGlyGluGlyThrThrPheTrpLeuAspSerSerSerVal	Qy 201 SerProTyrGluLeuHisValArgArgValAspValLeuProAspAlaGluGluVa	Qy 181 MetAlaAsnPheArgAspLeuAlaLeuAlaHisHisArgAlaArgArgHisGlyAlaAs	Qy 161 ProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGluIl	Qy 141 LeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHis	Qy 121 ProSerProPheThrAlaValArgTyrHisSerLeuAlaAlaThrAspLeuProAs:	Qy 101 PrometHisGlyArgValSerGluValArgHisThrGlyGluAspValPheArgGlyLeu	Qy 81 CysLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAlaProGlu	Qy 61 ArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeuGlyVa	Qy 41 ProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArgGlu	Qy 21 GlyGluAlaThrGlyGlnProProValValProAsnAspAlaAspTrpSerArgLeu	Qy 1 MetArgThrLeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIle 	/ Match: 100.00% Indels: 6 Gaps: 0-089-514-2 (1-686) x BD178313 (1-2061)	Pred. No.: 2.06e-166 Length: 2061 Score: 3573.00 Matches: 686 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1. /o.	producing the same and novel biosynthetic gene Location/Qualifiers CDS (1)(2058).	PC C12R1:645) CC Transformant producing PF1022 substance and proces
	LeuGlu 240 CY Db 1	Arg 220	p 200	e 180 Oy Db 1	ArgGluLys 160 Qy 5	140 QY 420 Db 1	Qy 461 	100	1 80 Qy Db 1 C 240	60 Qy Db 1	Oy 381 	20 Qy 60 Db 1	Qy 341 Db 1021	Оу 321 Db· 961	Оу 301 рь 901	Qy 281 Db 841		cess for CC Db 721
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	1 MetArgThrLeuleulleAsj ATGCGCACGCTTCTGATCGA	100.00% Indels: 6 Gaps: 0 x BD093914 (1-2061)	No.:	ORIGIN - Alignment Scores:	/dr /mc /or	CDS	C12N15/09, C12N5/		COMMENT OS Streptomyces venezuelae PN WO 0123542-A/1 PD 05-APR-2001 PF 29-SEP-2000 WO 2000JP006783	AL Pate	AUTHORS Yanai, K., Okakura, K., Yasuda, S., Watanabe, M., Miyamoto, K., Mido, N. and Murakami, T. Transformants that produce secondary metabolites modified by a functional functional functional model biographics.	ORGANISM Streptomyces venezuelae Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyceneae; Streptomycetaceae; Streptomyces. REFERENCE 1 (bases 1 to 2061)	VERSION BD093914.1 GI:22639502 KEYWORDS WO 0123542-A/1. SOURCE Streptomyces venezuelae	DEFINITION Transformants that produce secondary metabolites modified by a functional group(s) and novel biosynthesis genes.	RESULT 2 BD093914 2061 by DNA linear DAT 27 AUG 2002 LOCUS BD093914 2061 by DNA linear DAT 27 AUG 2002	Qy 681 AlavalAlaGlyAlaArg 686	Qy 661 GluGluPheThrGluThrValValLysAlaArgAlaMetValThrAlaLeuAspGlySer 680	Qy 641 AlaAspGlyGlnAlaGluPheGlyValGlyGlyAlaIleValSerLeuSerAspGlnGlu 660	
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translation="MTEQNELQRLRAELDALDGTLLDTVRRRIDLGVRIARYKSRHGV/
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A role for pabAB, a p-aminobenzoate synthase gene of Streptomyces
venezuelae ISP5230, in chloramphenicol biosynthesis
Microbiology 142 (Pt 6), 1345-1355 (1996)
96262706
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Bacteria; Actinobacteria; Actinobacteridae; Streptomyces.
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                                                                                                                             MetAlaAsnPheArgAspLeuAlaLeuAlaHisHisArgAlaArgArgHisGlyAlaAsp
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                                                                                                                                                                                         ProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGluIle
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87.53%
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                             ATGCGCACGCTTCTGATCGACAACTACGACTCGTTCACCCAGAACCTGTTCCAGTACATC
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Conservative:
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                                               AlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgProGlyThrSerThr
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                                                                                                                                                                                      GlyThrArgProArgGlyGlyThrAlaGluGluAspGluArgLeuArgAlaAspLeuAla
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Streptomyces vene:
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Sequence update by submitter
On Jun 5, 2001 this sequence
Location/Qualifiers
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The gene cluster for chloramphenicol biosynthesis in Streptomyc venezuelae ISP5230 includes novel shikimate pathway homologues a monomodular non-ribosomal peptide synthetase gene Microbiology 147 (Pt 10), 2817-2829 (2001)
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Bacteria; Actinobacteria
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He,J. Magazzo.
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/strain="ISP5230"
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	CDS 34986404 /note="non-ribosomal peptide synthetase; contains reductase-like domains near C-terminus" /codon_start=1	SDYTPEYFAKTRHAQESLGRFTMSDLDAFARAFTSGRMPRVVVSDTTFMRPEPDRWRW VPVRSARVFEDLKFLADRSWPGPPLLRWQYKRGFLSPGAAADVLDGLKQRIGASGGTP "
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Blanc,V., Thibaut,D., Bamas-Jacques,N., Blanche,F.,
Barriere,J.-C., Debussche,L., Famechon,A., Paris,J..

Dutruc-Rosset,G.

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Streptomyces pristinaespiralis 4-dimethylamıno-u-puro, pape, papM) genes, complete precursor biosynthesis (papA, papC, papB, papM)
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Streptomycineae; Streptomycetaceae; Streptomyces.
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                                   CTGCCCGACGACCAACTGCCCGCCCTGGAC--
                                                                  AlaProAlaGluProThrProAlaMetValPheGlyIleProGluAlaAlaAlaGlyPhe
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                                                                                                                                            pab gene.
Streptomyces griseus
Streptomyces griseus
                      biosynthesis
Gene 126 (1)
                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 4607)
                                                                                                                                                                                                                     Streptomyces griseus
M93058
                                                      synthase,
                                                                                      Criado, L.M.,
                                                                                                                                                                                                      M93058.1 GI:153396
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      93231527
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                                                                  ado,L.M., Martin,J.F. and Gil,J.A. pab gene of Streptomyces griseus,
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COMMENT
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Best Local Similari
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                                                    1370 ATGCGCACCCTTCTCGTCGACAACTACGACTCGTTCACCTACAACCTCTTCCACTACCTC
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                    21
GlyGluAlaThrGlyGlnProProValValValProAsn---AspAlaAspTrpSerArg
                                                                   MetArgThrLeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIle
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x STMPABA

(1-4607)

20

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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AATEDTADAVAGTLITACPLTHCFGLOSAYSALFRAGRQVLLSGWDVGRFLELARRER
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APLLRLLDTAFPGRERPGKDLDGEPDDGTDAGAPKDLVLPG"
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Location/Qualifiers
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354 CysTyrLeuLeuAlaLeuAspArgArgGlyHisAspAspGlyAlaArgAlaTrpLeuArg 373 1	ν ω	314 TYTLEUGIYTYTGIHLEULYBALBGLUTNTTNTGLYASPTOALBHISATGSETPTOHIS 333	GGGCTGCGCACCGAGGTGCCCGAACTTCCCTTCGCGTTCGCGCTCGGCTGGGTCGGC	294 ArgArgArgValProValAlaProGluLeuProPheGluPheAsnLeuGlyTyrValGly 31	2252 GACGGCGCCAGCACGGTCGAGAGAGCGCCTTCCTGACCTGGCTGG	AspClVThrThrThrAraThrAraAraBraDraDbaDbaDanTvrIonClnClnClnClnClnClnClnClnClnClnClnClnCln	254 ProLeuAlaGluTyrLeuThrTyrArgValAlaAspGlyValValSerValArgGlySer 273	2135 GACAGCAGCCGTCCCGGGGGCGAGCTGGGCCAGCTCTCCATGATGGGCGACGCCTCAGGT 2194	234 AspSerSerSerValLeuGluGlyAlaSerArgPheSerPheLeuGlyAspAspArgGly 253	219 ValArgArgGlyCysLeuProGlyGluGlyThrThrPheTrpLeu 233	2030 ACCCCACGGCGCTCCGGGTCATCGCAAAGTCGCTGCCCACGCGCTGGGACGCCGAGGTC 2089	201 SerProTyrGluLeuHisValArgArgValAspValLeuProAspAlaGluGlu 218			1910 CTGCTGGCCAACTTCCGCGACCTCACCGAGCGCCACCGCCGAACGGCCGACCGG 1969	O I Jewet A Jahen Dhohrnhent on A Jahran A Jahran A Jahran Jahran Communication on A Jahran A	160 LysbroLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGlu 179	0	140 GluLeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArgGlu 159		LeuProSerProPheThrAlaValArqTyrHisSerLeuAlaAlaThrAspLeuProAsp	100 GlubroMetHisGlyArgValSerGluValArgHisThrClyGluAspValPheArgGly 119 		80 ValCysLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAlaPro 99	ccaccaactrcaaccreracacccaarcaccaagaagaaccaactaccaaractraac		40 LeurrovalGluAsphraAspAralleValValSerProGlyProGlySerProAspArg 59	TCCCGGGCCAACGGCCGGGAACCCGAGGTCATCCGCAACGACGACCGGCCTGGCGGCCG 1
ACCESSION VERSION KEYWORDS	RESULT 9 SGR300302 LOCUS DEFINITION	₽	Ş	₽ 5	₽b	Qy	B 1	Ş ₽	γ	Db !	Q 5	ş Ş	DЬ	Ş	Ф	β	Db :	Q E	\$ 5	망	9	₽,	ν _ο	물 4) B	ş	90	δ

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	MetValThrAlaLeuAsp 678 :::::: CTGCTGCGTCTCCTCGAC 343	IleValSerLeuSerAspGlnGluGluGluPheThrGluThrValValLysAlaArgAla 672	IleValIleArgThrIleValLeuAlaAspĠlyGlnAlaGluPheGlyValGlyGlyAla 652	ArgGlyValTyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSer 63	MetThrGlyAlaProLysLysArgThrMetĠluIleIleAspArgLeuGluGluGlyPro 6	ArgLeuArgProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySer 59	ArgLeuPheGluValGluThrTyrAlaProValHisGlnLeuValSerThrIleArgGly 572	ValAspLeuValArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValPro 55	GluargLeuArgAlaAspLeuAlaGlyArgĠluLysAspArgAlaGluAsnLeuMetIle 53	GlyValGluSerLysProIleLysGlyThrArgProArgGlyGlyThrAlaGluGluAsp 512	ProGluLeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAepGly 49 :::::	ProLeuTyrSerAlaLeuArgAlaIleSerProValProTyrGlyAlaLeuLeuGluPhe 47	GluSerTyrGluIleCysLeuThrAsnMetValThrAlaProThrGluAlaThrAlaLeu 4	HisasplysaspalaTyrLeuLysargIleAspGluCysLeuLysGluIleArgAsnGly 4	MetValPheGlyIleProGluAlaAlaAlaGlyPheGlyProLeuAlaArgAlaArg 412	GluThrAlaGluThrLeuThrGlyLeuAlaValArgAlaProAlaGluProThrProAla 3 :::

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SGR300302

39314 bp DNA linear BCT 20-MAR-2002 Streptomyces griseus partial ORF1, canA gene, canC gene, canF gene, canT gene, canRA gene and canRB gene.
AJ300302

AJ300302.1 GI:12231153

ABC-transporter; aminotransferase; can RB gene; canA gene; canC

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REFERENCE
AUTHORS
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cytochrome P-450; ferredoxine; PABA synthase; thioesterase.
Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-NOV-2000) Gil J.A., Mic
Leon, Campus de Vegazana s/n, 24071,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thesis
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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71, SPAIN
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13190. .15361
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_xref="GOA:Q9EWC0"

/gene="canRA" 20829. .21836

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                                                                                                                                         GluLeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArgGlu
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                                      CTGCCGCTGTGGGGAGTGCAGTTCCACCCCGAGTCGGCACCCAGGACGGCCACCGG
                                                            LysProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGlu
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ADRLADRIAVLSAGRVVAAGTAPELKATVGRRTVTLTLETGEDVSAARTALRGAGFAP
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21970. .22776
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GluArgLeuArgAlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIle
                                                                         GGTCCCATGGCCGTGCTCAGCAGCTCTCCGGAGCGGTTCCTGCGCATCGACCGGCACGGG
                                                                                                                                               ProGluLeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAspGly
                                                                                                                                                                                              GCGGCCTACCGCGCGCTGCGCCGGGTGAGCCCCCCCCGTTCGCCGCGTTCCTGGACTTC
                                                                                                                                                                                                                      ProLeuTyrSerAlaLeuArgAlaIleSerProValProTyrGlyAlaLeuLeuGluPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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                                                                                                                                                                                                       Direct Submission
Submitted (30-MAY-2003) Bio-X Life Science Research Center,
Shanghai Jiaotong University, 1954 Huashan Road, Shanghai
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AY310323
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Bacteria; Actinobacteria; Actinobacteria; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 138203)
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AVAERHELTVLCRVAS FLRHDDADLD VL-PVPAL-PDA VHNPA VAGVWAWEHGVAGVHRE
EVRRLARS AF VPAATGR PLL-VVPRLLGGRALLLTDGOBE AGNICAGLLDES HRRRAA I
SVAH I LTVRAELH I RIGR PDAAARDLAAAQAEL PLDR LHPL FU PWLALSMITDLQNG
HTERARETAAR PL-P LAHESATTAQULF RAGVLARTDDEPIQAEEHFRA GGRULLHG
CANPAVQPWRSLAAEAAHTLGDTEEAARLVHEBVRLARRWGAAAPLGRAQLSLAVVTE
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13522. .14898
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KATLPDI LRRTEGLTPQPGDTPAQRQQLAMLS VLSAAEGGGAEETVGRARRALRAPGV
PLGVWSLLPTSLALSLADENEAAEEVLETVLRGSGDTAAVWTY VLALSTRSLFRLENG
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PPGPHVPSAVARPPGPRPAVLTGRRTAKAPGHDAAVMHGLTAVERETAALAAQGLGNR
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attachment"
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Best Local Similarity:
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                                                                                                       180 IleMetAlaAsnPheArgAspLeuAlaLeuAlaHisHisArgAlaArg------ 195
                                                                                                                                                                                                                                      140 GluLeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArgGlu
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---ArgHisGly----
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                                                                                                                                                                                                                                                                                       CTGCCGCAGCCGCTGGAGGTGGTGCGGTACCACTCCCTCGCGGTGACGGAACTGCCGCCG 19029
                                                                                                                                                                                                                                                                                                                                                              GAGCCCCGTCACGGCCGCACCTCGGCGGTACGGCACGACGGCACCGGGCTCTTCGAGGGG
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Q B Q	Db Qy	Db Qy	Db Qy	g Q	Db Qy	dg VQ	g 99	dg VQ	Qy	D Qy	do do	g Q	φ φ	B &	Qy da	Qy dd	Db
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AP006618_36 3600001 3710000 AP006618_37 3700001 3810000 AP006618_38 3800001 3910000 AP006618_39 3900001 4010000 AP006618_40 4000001 4110000 AP006618_41 4100001 4210000	3200001 331 33 3300001 341 34 340001 351 35 3500001 361	200001 291 2900001 291 300001 301 31 300001 311	24 2400001 251 25 2500001 261 26 2600001 271	2000001 211 21 2100001 221 22 2200001 231 22 2200001 231	16 1600001 171 17 1700001 181 18 1800001 191	12 1200001 131 13 1300001 141 14 1400001 151	00001 800001 91 00001 101 1000001 111	0.000 400001 51 0.00001 51 0.00001 61 0.00001 71	Name Begin Bi	it into 61 fragments	Qy 672 AlaMetValThrAlaLeuAsp 678 Db 20659 CCGCTGCTGCGTCTCCTCGAC 20679	Qy 652 AlaIIeValSerLeuSerAspGlnGluGlubleThrCalWalWalLysAlaArg 671 :::::::	Qy 632 SerIleValIleArgThrIleValLeuAlaAspGlyGlnAlaGluPheGlyValGlyGly 651 ::: ::: ::: :::	Qy 612 ProArgGlyValTyrSerGlyAleLeuGlyTrpPheAleLeuSerGlyAleAleAspLeu 631	592 SerMetThrGlyAlaProLysLysArgThrMetGluIleIleAspArgLeuGluGluGly 61	Qy 572 GlyArgLeuArgProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGly 591	Db 20299 GACCCGGTGTTCCAGGTCGAGACGTACGCGACCGTGCACCAGCTGGTCAGTACCGTCACG 20358

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AUTHORS
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TITLE
JOURNAL
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                                                                                                                                                                      Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nostoc sp. PCC 7120 DNA,
AP003593 BA000019
AP003593.1 GI:17132540
                                                                                                                                                                                                                                                                                                                                                                           Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120 DNA Res. 8 (5), 205-213 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura
Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A.,
Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M.
Yasuda,M. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nostoc sp. PCC 7120
Nostoc sp. PCC 7120
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                                                                                                                                                                                                                                                                                                                   Kaneko, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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                                                                                                                                                                PCC
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                                                                               34009 CCAGCGCCATCCCAAGAATTTACTGTTTGTAGCCAAAAACTAGATTATTACCTTGATACA 34068
                                                                                                                                                                                                                                                                                    33895 TATAAATTGCTGGAAAACTTCCAA-----GCCATTACGGAAGGATTCATCCGCCAAAAT 33948
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GluGluValArgArgGlyCysLeuProGlyGluGlyThrThrPheTrpLeuAspSerSer 236
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           GACATGGACGCAACCGACTGCATTCGTCTGGCATTTCCCGGGCGCCTCGATGACAGGTGCG
                                   GlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAla
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                                                                                                  GTAGAAAGTTATGCAACGGTGCATCAACTTGTCAGCACTATCCGTGGTTTATTATCCCCC
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acyl-coA ligase; aurA gene; aurB gene; aurC gene; aurD gene; aurE gene; aurF gene; aurG gene; aurH gene; cytochrome P450;
N-oxidase; O-methyl transferase; PABA synthase; polyketide synthase type I; transcriptional regulator.
Streptomyces thioluteus
Streptomyces thioluteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STH575648 29132 bp DNA linear Streptomyces thioluteus aureothin biosynthesis gene (aurABCDEFCHI genes), strain HKI-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JUL-2003) Hertweck C., I
Hans-Knoell-Institute, Beutenbergstr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iteration as programmed event during polyketide assembly; molecular analysis of the aureothin biosynthesis gene cluster Chem. Biol. 10 (12), 1225-1232 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/codon_start=1
/transl_table=11
/product="PABA_synthase"
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[1745. .13832
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                                                                                                                                                                                                                                                                                         Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center, 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax.81-3-3481-824)
This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*4), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3)
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Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
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Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
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Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                      Following url is also available. http://avermitilis.ls.kitasato-u.ac.jp.
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Omura, S., Ikeda, H., Is
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                                                                                   *3 The KitaBato Institute

*4 National Institute of Technology and Evaluation

*5 School of Science, KitaBato University

*6 Institute of Medical Science, University of Tokyo

*7 RIKEN, Genomic Sciences Center
                                                                                                                                                                                                   *1 Kitasato Institute for Life Scien
*2 National Institute of Infectious
                                                                                                                                                                                                                                                     J. Ishikawa.
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                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTGGAGFIG$HFVRRLLTGAYPAFTGAEVVVLDKLTYAGRLENLAPVLGSPSLIFVHGDICDGPLYADLMOGSDMVHFAAESHVDRSVADAAEFVRTMVLGTHTLLRAATDAAVDRFVYISTDEVYGSIDSGSWHFAAESHVDRSVADAAEFVRTMLARSFHTHGLLRATTDAAVDRFVYISTDEVYGSIDSGSWWFDAPLEPNSPYSASKASSDLLARSFHTHGLDVIITRCSNNYGHHOPEBKLIPRFVTHLLNGTKVPLYGDGENVRDMLHVDDHCRGIALVAERGRPGEIYHIGGGTELSNRELTARLLDLLGVDMSMVEPVTDRKGHDRR
                                                                                                                                                                                                                                                                                                                                         complement (3187. .4086)
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/gene="aveBII"
/note="SAV946
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AFVGPCLGKRRGLGEWTPPGSGHÞVVLISLGTVFNRQLSFFRTFVRAFTDVPVHVVIS
LGKGVDPDVLRPLPPNVEVHRWVÞHHAVLEHARALVTHGGTGSVMEALHAGCPVLVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="glycosyl transferase"
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979. .2217
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                                                                                                                                          /codon_start=1
/transl_table=
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/protein id="BAC68656.1"
/db_xref="GI:29604587";
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GGHIVTVASAAAFQPTRAVPAYATSKAAVLMLSECLRAEFAEFGVGVSVVCPGFVRTS
                                                                                                                                                                                                                                                        gene="aveBIII"
                                                                                                                                                                                                                                                                                                               /gene="aveBIII"
                                                                                                                                                                                                                                                                                                                                                                                               /SLDISKISAELGYAPRVPFEEGLAQTVQWYVENRTLWEPLTARPELPVSDGASGAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="aveBII"
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/transl_table=11
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208. .921
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NCIMB 12804 or NRRL 8165.~synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="SAV945
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/db_xref="GI:29604585"
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/transl_table=
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/gene="aveBVII"
complement (7442. .8215)
/gene="aveBVII"
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ARGRALDFVVDLRTGSPTFGQWDSVLLDQERFRSVYLPTGVGHAFVALEDDTAMVYLM
SSGYYVQNEHALSPEDPDLALPLGHHLGRAPTLSERDRRAPTLQQALRRGMLPEYRAS
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ELARWPVLLRLVARREGVVPPGGAAETETRTADLTAASSVALAVTDADVVIHLVARLT
GGAAWRAAESDPVAERVNUGVMEDVVAALRSGRRAGPPPVVVPAGSVYQOGRPGRVDG
SEPDEPVTAYARQKLDAERTLKSATVEGVLRGISLRLFTVYGAGPGPQGNGVVQAMVL
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VHGGAAVKYLEYFTQPRRATVVVDVLQSEHGAWFHRKFNRNIVVETDEDVPLDDDFRW
LTLGQIGELMHRDNLVNMDARTVLACLPTPFDEPAALHSDAELLSWYAAERSRHSVHA
                                                                                                                                                                                                                                                                                                                                                                                                                   /protein id="BAC68660.1"
/db_xref="GI:29604591"
/translation="MSVRADADHTEPSTAHRAARRPARVPRPLRRRGRHRRRTSLDA
FTGMWTRRSGAHRFRVERIPPHGMDAWSFHPGTGNLAHRSGRFFSVEGLHVRGGEQPF
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PTAPRSNLAITGLYLYDNDVIEVARGIRSSARGELEITDVNRAYLAEGRARLVDLGRG
FTWLDAGTHDSLMHAGQYVQVLEKRQGVRIACLEEIAFRMGLIDADDCYLRGVELAGS
                                                                        /product="dTDP-6-deoxy-L-hexose
/protein_id="BAC68661.1"
/db_xref="GI:29604592"
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/product="dTDP-4-keto-6-deoxy-L-hexose
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/note="SAV948
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/db_xref="GI:29604590"
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/product="dTDP-4-keto-6-deoxyhexose 3,5-epimerase"
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gArgProPhePheAsnTyrLeuGluGluGlnLeuGluArgArgArgValProValAlaPr 301
                                                         CGACGTCGAGAGCGGCCTCTGTGAGATCGAGCGGCCCGGGCGGCCCGTGCGCAAGGTCAG
                                                                                            rArgValAlaAspGlyValValSerValArgGlySerAspGlyThrThrThrArgThrAr
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                                                                                                                                                       yAlaSerArgPheSerPheLeuGlyAspAspArgGlyProLeuAlaGluTyrLeuThrTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-MAY-2002) Director'General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-066, Japan (B-mail:bio@nite.go.jp, Tel:81-3;3481-1933, Fax:81-3-3481-8424) Kawarabayasi, Y is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan
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Corynebacterium efficiens YS-314
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Director-General of Biotechnology Center.
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/product="hypothetical protein"
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/translation="MDQAPSGCLVDCVHGYIFYDTPVPMLLFPVGTSGNRKIVLDLFN
/translation="MDQAPSGCLYGMVIGLFTBWHTHYYVCVVFCGEFDDGSGRTLAAC
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/gene="rrnA_16S"
/product="16S_ribosomal
                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="YS-314"
                                                                                                                                                                                                                                                                                                                     db_xref="taxon:196164"
                                                                                                                                                                                                                                                                                                                                                                                      organism="Corynebacterium"
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, Kimura, Ikeo,K.

,Ε.,

BCT

and

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SdO
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                                                                                                                                                                   Sac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transT_table=11
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/db_xref="GI:23492727"
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PMLEIASQQTLGCGNNQYSGGRGDLGLETAVASDRHKRFKLDYDDTEVLITVGATEAI
SASVLGLVEPGDEVIVLEPYYDAYAAAIALAGATRVAVPLKEEDNTWVLDTDAVHAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5925. .7088
/note="CE0889, similar to AX063829-1|CAC25156.1| percent
identity: 79 in 387 aa"
                                                                                                                               complement(9548. .11851)
/note="CE0892, similar to
                                                                                                                                                                                                               GREGDVFSLIGPKRYDAPWKDLEAQGFIATADCVEVRTTMTDAERMYYATAETADRYR
LAATAHTKTRVVRRILEQHQGQPTLIIGAYLDQLEELGAEFDAPIVDGKTSNKKRGEL
FDRFRSGELNVLVVSKVANFSIDLPEAAVAIQVSGTFGSRQEEAQRLGRLLRPKADGG
                                                                                                                                                                                                                                                                                             HPAHGLILESSEPAILVEISRHRKIKPMLGQQLDPETIAVHPSERGRLKQELLKIGWP
AEDLAGYVDGEAHPIALSTEVEDWSLRDYQQYAADS FWBGGGSGVVVLPGGAGKITWVGA
ASMARAQATTLILVTNTVAGRQWKDELLRRTTLTEDBIGESYGGERKEIRPATTATYQV
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/translation="MAFGDGPLIVQSDKTVLLETGHDLAGEARAALAPFAELERAPEH
/translation="MAFGDGPLIVQSDKTVLLETGHDLAGEARAALAPFAELERAPEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="mTHFSFDVDEAYARKNNEFLRDTKRLQISAFFFGLVLLAIGGVL
YYLADGAVWGWMVLIVMGIMAALSFVMIPVLPRQVGSAESLYNTYPLVPAVVAEINPR
DVVLLALVNTNVDETLPPRWGLAVRTINRLGVHDRKLGERVPSVAVSGRRTIRDQDHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKKTSMIINSPHNOTGSVFSKRSLEALAGIARAYDLLVLSDEVYEHLTFDKVSHTAV
ASLPGMMDRTITVSSAAKTFNOTGMKTGMALAPAPILEAVIRAKQFMSYVGATPFQPA
VAHAVAHEKBWYKQMKRGLQNKRDILTDALTQAGLKYHBSHGTYFVVADIGERGGAEF
CFDLIDRVGVAAIPVQAFVDKPEQMSSKVRFAFCKQEDTLREAAQRLRAAGSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5606
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/transl_table=11
/product="conserved hypothetical protein"
/protein_id="BAC17702.1"
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identity: 75 in 547 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(7822. .9495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEISPMPITWGTTDADVVRRAEKTIPHDLWNKLEKNRNRLDEVKNTRMNLLVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
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/db_xref="G1:23492728"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7180. .7821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2399. .5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       " NNPPHEHSPWWVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="CE0890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="rrnA_5S"
/product="5S_ribosomal_RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="BAC17696.1"
/db_xref="GI;23492724"
                                                                                                         dentity: 36 in 741 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="CErRNA03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="CErRNA02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="rrnA_23S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSSQTPNSMPPTYHHHLGDVFADPWVMIHPITTCWWQPHPGSNT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="23S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e"rrnA_58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrnA_238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2215)
                                                                                                                                  AE006976-11 | AAK45126.1 | percent
                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                            SCOre:
                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                    No.:
1.6e-64
1541.00
60.71%
50.52%
43.13%
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IPQLIKAGLLSKVDEQTVKLPGVVRRVLEGQEDTAWRVVPVEPSAVPGADDÄGIAÄGLEVARLORMLIDALSTARASTLKEGALGVRMVTRLTRELQVDEQOVARVVSLGYSSGLLROVARLORMLIDALSTARASTLKEGALGVRMVTRLTRELQVBEQOVARVVSLGYSSGLLROGVDEPLPADDDGGDYIAPTEVADEWLQATLAEQLAHLIAEQTAYAWTQYAAWLVGEADE KNEPHHLLSPASRRDALFETRAWILGSLTRVGEEDLEADLFFHHPLAASRIPRETIRH LLEEARWIGAVAGGGVTSPARVLTQAPAGVIPEIADIAVAVRAPKPVDYFIVQADYTV MYPGFLOPEMOKIIGQLADLESPGLASVYRISBASLAHAMDLGLTATEIEDFITQHSATGLEPGNAYLLGDIARRHGTLRGGPALCYLRSDDPALLHSAVEAGALGLRQIAPTVAVSNASLIEVTTALRKAGMQPVAEDALGASLDLARRAPRARVPAARGOPRSAGPLDESRIRAVSVASLIEVTTALRKAGMQPVAEDALGASLDLARRAPRARVPAARGOPRSAGPLDESRIRAAVVAAIRREEVARTGTVSDQPTLAVLQAAVRGQRTVTLGFVDKQGVAVHRTVKPLTVNAQQVDALDESTGAVHRFMLHRITEVIVD"
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TVSITASSPAGEIEVFPYSICEPGVECAENEVPTLEVGADEELRLTIPEIIHDHDWYL
LTIYDDPAANDEFYHTSYETTEVTVPGSVDPVTEGGERPRLVVVEVTSVMIGTDDNGE
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RIEFDFAAGRKGPQALRVKVLETPRRRPQHTYKPEELNGIISDMVTMLEGTVQPALLK
GHYPDRKVGEQVAKILRAVAKELEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mlfmgrhsaktatpfvkmaattvafgaaavafapaasaapdsdw
Drlancesggnwaintgngyhgglqfspstwrayggdefapfayqatreqqiavaert
Lagqgmgawpacssklglnsaptprnlnpapapapapabayratvdtntnpvvgss
Dlntvqgiydavsgtlaqygvqvpaeiqahynafigr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGNMANVEKKGYVDPAWPDHDPSEGHVVTELIAPYAGASSPWGD
DMEFPVPAETIGYVHPYTRINR"
Complement(12229. 12822)
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identity: 71 in 195 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11836. .12036

/note="CE0893, similar to AL583924-91|CAC31110.1| percent identity: 50 in 62 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPCFPF8QIRQTKVTSTAPKLGDIMKKDSPVPTLTGWLEQLDDD 
QLSGILRURFDTALFLEPGLGSLAARLQLRAS!QRAVHCLSALELAVLEAANAGGEL 
NPITAPEVVERLHRALRHSAAVFTABO]GEALMARLRQLALVFGGERFILLETTMATLF 
TNWQLLPEEHGRSLTFGEASQSIEALFARHRKILVTLVTSNGLGLTRDAALSADFARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (13881. .14408)
                                                                                                                                                                                                ETPYTTTWSLATVEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative cold (
/protein_id="BAC17705.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="CE0895, similar to AE006977-4|AAK45135.1| percent
identity: 52 in 127 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="BAC17704.1"
/db_xref="GI:23492732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical
/protein_id="BAC17703.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
product="putative"
                                  /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="CE0896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1/
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="BAC17703."
/db_xref="GI:23492731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="GI:23492730"
                                                                                         dentity: 40 in 267 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .13725
glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cold shock protein"
                                                                                                                                  AE001874-1 | AAF09704.1 | percent
cyclotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein"
```

Matches: Conservative: Mismatches: Indels:

 360	341 AlaAspArgAlaIleAlaLeuAspHisGlnGluGlyCysCysTyrLeuLeuAlaLeuAsp 	Ş
 340 185796	321 AlaGluThrThrGlyAspProAlaHisArgSerProHisProAspAlaAlaPheLeuPhe	g 9
ω (83 CCGGGGGTGGGTTTCCGCCTGGGGTGGGTGGGATACCTCGGGT	_
185682	GAGCTGTTCGACTGGCTGCGGATGATGTGCGTCGCAACCGCGTIII GAGCTGTTCGACTGGCTGCGTGATGATCTGCGTCGCAACCGC	\$ ₽
300	luGluGlnLeuGluArgArgArgValPr ;;;	ş
280 185634	261 TYRATGVALAIBABBGTYVALVAISETVALARGGTYSERABBGTYTNTTNRTNRARGTNR ::: :: 185617 CACCGGGTGGGGGAGGGG	₽ &
œ	66 GGCACCACCTATATGGGTGA	, B
260	ArgP	ş
185565	185515 GAGACGCTCTTCGCCGGGTCGGAGCACGCGTTCTGGCTCGATGATCCGCAG	B &
- 00	61TGGGÁGATCACCGAGCATGTGGTGGAGACAAGCGTCGÁCCCGGCGGCGGCGGTGT	?
220	rProTyrGluLeuHisValArgArgValAspValLeuProAspAlaGluC ;;; ;;	ş
185460		망
200	rgA	δ
180 185418	161 ProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGluIle	B 8
185358	185299 CTGGAGGTCACCGCGAGGACCGGGGATCATGGCGCTGCGCCACCGCGAGCTG	В
160	ıProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArc	ş
185298	185239 CCGCCCAGTTCGACCGCTCCGTTACCACTCCCTGGTGGCCACCGATCTGCCGCCGGAA	₽ \$
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120 185238	101 ProMetHigGlyArgValSerGluValArgHisThrGlyGluAspValPheArgGlyLeu	B 8
100 185178	81 CysLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAlaProGlu	g 9
185118	9	В
80	61 ArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeuGlyVal	ઠ્ઠ
185058	184999 GACGAGACGCTGTTCGACGCCGTCATCATCTCACCCGGCCCCCGGGCCACCCCGGGGTGGCG	В
60	41 ProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArgGlu	Ş
40 184998	21 GIYGINALBITATELYGINEOPYOVALVALFEORAGABARABARDTIPSEERAEGLEU 	용 성
,		?
20 184947	1 MetArgThrLeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIle	<u> </u>
	89-514-	US-10-0

G	100000	5
	1000	, c
1 GluGlupheThrGluThrValValIvsBlaBroBlaMerValThrBlaGeu 677	2	5
ACCCCCGGCGTCTGGAGTACGGGGTCGGCGGGGCGATCCTGGCCCTGTCGGACCCCGCC 18	18662	문 4
-	Λ 4	5
::: ::: :::	Db 186568	U
	Qy 621	o
	Db 186508	U
)1 ThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyrSerGlyAlaLeu 620	Qy 601	ю
	Db 186448	В
N AlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLysLysArg 600	Qy 581	ю
-	Db 186391	
il AlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgProGlyThrSerThr 580	Qy 561	ю
	Db 186331	ы
AsnSerValCysAlaIleGlySerValHisValProArgLeuPheGluValGluThrTyr 560	Qy 541	n
	Db 186271	ы
1 GlyArgGluLysAspArgAlaGluAsnLeuMetIleValAspLeuValArgAsnAspLeu 540	Qy 521	0
	Db 186211	ы
)1 GlyThrArgProArgGlyGlyThrAlaGluGluAspGluArgLeuArgAlaAspLeuAla 520	Qy 501	n
	186	ы
	Оу 481	0
)1 GCCAACCCCACCTCCTATGGATCATTCCTGCAGCTGGGGGAGATGGCGGTGCTGAGCTCG 186150	Db 186091	ы
	Qy 461	0
	Db 186031	п
11 AsnMetValThrAlaProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeuArgAla 460	Оу 441	0
	Db 185971	ы
21 ArgīleAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCysLeuThr 440	Qy 421	
	Db 185911	-
)1 AlaAlaAlaGlyPheGlyProLeuAlaArgAlaArgHisAspLysAspAlaTyrLeuLys 420	Qy 401	0
33 CAGCTGCCCCGT 185910	Db 185893	н
31 GlyLeuAlaValArgAlaProAlaGluProThrProAlaMetValPheGlyIleProGlu 400	Qу 381	0
SI GAGCAGGGGAAGTGGTTCGCGGAGATGACCGCCGCCCTGGGG 185892	Db 185851	п
31 ArgArgGlyHisAspAspGlyAlaArgAlaTrpLeuArgGluThrAlaGluThrLeuThr 380	Оу 361	_
97 GCCGACCGGGCCATCGCCATCGAACCCGGCCGCGTGTGGCTCATGGCGCTCGGT 185850	Db 185797	н

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Result
No.
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-Q=/cgn2_1/USPTO_spool_h/US10089514/runat_04102005_105743_8027/app_query.fasta_1.1621
-Q=/cgn2_1/USPTO_spool_h/US10089514/runat_04102005_105743_8027/app_query.fasta_1.1621
-DB=N_Geneseq_-QFMT=fastap_-SUPFIX=rng_-MINMATCH=0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TFRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENO -NAXLENO200000000
-USER=US10089514_GCGN_1 1_860_@runat_04102005_105743_8027 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WART_DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                       29-SEP-1999;
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Aah68527 C glutami
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ALIGNMENTS

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29-SEP-2000; 2000WO-JP006783
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                                                                                                                                                                                                                                                                                                                                                4-amino-4-deoxychorismic
                                                                                                                                                                                                                                                                                                                                                                                                               4-amino-4-deoxychorismic acid synthase, papA, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001 (first entry)
99JP-00276314.
                                                                                                                                                                        /*tag= a
/product= "4-amino-4-deoxychorismic
                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              chorismic acid; p-aminophenylpyruvic acid;
smic acid synthase; enzyme; papA; ds.
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CC as to produce a secondary metabolite. The secondary metabolite has a CC benzene ring skeleton free from substitution at the para-position by a CC nitrogen-containing functional group, thereby enabling the production of CC a secondary metabolite with a benzene ring skeleton substituted at the CC para-position by a nitrogen-containing group. The transformant organism CC of the present invention has been produced by transferring a gene CC participating in the biosynthesis pathway from chorismic acid into para-position the present sequence is the coding sequence for 4-amino-4-deoxychorismic acid synthase (paph), from Streptomyces CC venezuelae. paph participates in the biosynthesis pathway from chorismic codi into p-aminophenylpyruvic acid, and so the paph gene can be used to produce the transformant of the present invention. The transformant can cc be used to produce metabolites for application in pharmaceuticals, CC veterinary drugs and agrochemicals
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Best Local Similarity:
Query Match:
DB:
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Murakami
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The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-tRNA with at least one unnatural amino acid in the translation system and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Asp12TAG mutant of chloramphenical acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid containing the individual genes papABC that encode

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Page 127-128; 188pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition useful for producing protein comprising unnatural amino acid, has translation system comprising orthogonal tRNA and orthogonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase; ds; plasmid;
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06-FEB-2002; 2002US-0355514P
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A, Pastrnak M,
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Santoro SW,
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697 GGCGCCTCGCCGTTCCTCCTCGGCGACGACGCCGCC 261 TyrArgValAlaAspGlyValValSerValArgGlyS 1	Qy 221 ArgGlyCysLeuProGlyGluGlyThrThrPheTrpLeuAspSerSerValLeuGlu	Qy 201 SerProTyrGluLeuHisValArgArgValAspValLeuP	Qy 181 MetalaasnPheArgAspLeuAlaLeuAlaHisHisArgAlaArgArgHisGlyAlaAs	Qy 161 ProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGluIle	Qy 141 LeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArgGluLy	Oy 121 ProSerProPheThrAlaValArgTyrHisSerLeuAlaAlaThrAspLeuProAspGl:	Qy 101 ProMetHisGlyArgValSerGluValArgHisThrGlyGluAspValPheArgGlyLeu	Qy 81 CyeLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAlaProGlu 	Qy 61 ArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeuGlyVal	Qy 41 ProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArgGl	Qy 21 GlyGluAlaThrGlyGlnProProValValValProAsnAspAlaAspTrpSerArgLeu	1 MetArgThrLeuleulleAspAsn 1 ATGCGCACGCTTCTGATCGACAAC	/ Match: 87.53% Indels: 8 Gaps: 9-514-2 (1-686) x ABZ69799 (1-3305)	Pred. No.: 4.38e-213 Length: Score: 3127.50 Matches: Percent Similarity: 91.00 Conservative: Best Local Similarity: 90.09 Minnatches:	SQ Seguence 3305 BP; 445 A; 1327 C; 1121 G; 412 T; Alignment Scores.	CC the enzymes used to carry out the conversion of CC unnatural amino acid p-aminophenylalanine (pAF)
D H U-	Oy	roAspAlaGluGluValArg 220 	Qy gAlaArgArgHisGlyAlaAsp 200 Db	Qy ySerAspPheGlyArgGluIle 180	Qy 	u 140 - 396	120 336	YThrValGlyLeuAlaProGlu 100	80	177	Qy 	Qy	17 Qy 3	3305 Qy 618 Db	0 U; 0 Other; Er	chorismate to the
1750 CCCATGGAGATCATCGACGCCTGGAGGAAGGCCCCCGGGGCGTCTTACCCGGGGGCGTC 1809 621 GlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIleArgThrIleValLeu 640	581 AlaAlaCysValArgAlaAlaPheProGlyGlyGlyGerMetThrGlyAlaProLysLysBarg 600	61 AlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgProGlyThrSerThr	41 70	21 10	01 50	81 SEPPTOGINATGPREHENINTITEGJYALBASDGJYGIYVAIGINSETLYSPTOLIELYS 90 TCGCCCGAGCGGTTCCTCACGATCGGCGCGCGCGCGGCGTCGAGTCCAAGCCCATCAAG	61 IleSerProValProTyrclyAlaLeuLeuGluPheProCiluLeuSerValLeuSerAla 4	41 70	21 ArgileAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCysLeuThr 4 :::	01 AlaAlaAlaGlyPheGlyProLeuAlaArgAlaArgHisAspLysAspAlaTyrLeuLys 4 	381 GlyLeuAlaValArgAlaProAlaGluProThrProAlaMetValPheGlyIleProGlu 400 	61 57	341 AlaAspArgAlaIleAlaLeuAspHisGlnGluGlyCysCysTyrLeuLeuAlaLeuAsp 360 	321 AlaGluThrThrGlyAspProAlaHisArgSerProHisDroAspAlaAlaPheLeuPhe 340 	77 CCCGACCTGCCCTTCGAGTTCAACCTCGGCTACGTCGGCTACCTCGGCTACGAGCTGAAG	817 GCGGCGACCCTCTTCAGCTACCTGGAGGAGGAGCTCGAACCGCCGGGGGGGTCCCCGTCGCC 876

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RESULT 4
ABZ69798
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                                                                                     Percent Similarity:
                                                                   Local
                                                                                                                                                                                                                                                     and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Asp12TAG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is provided exogenously. The translation system is a cell and the unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid for use in the biosynthesis of p-aminophenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-tRNA with at least one unnatural amino acid in the translation system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; TyrRS; orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase; diosynthesis; p-aminophenylalanine; pAF.
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                          sequences from the Coryneform bacterium Corynebacterium glitamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office
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07-APR-2000;
03-AUG-2000;
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Tateishi N,
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                                                                                                                                     MetArgThrLeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIle
                                                           GAAGAGGTTACGGGTCAGGCACCTGTGGTGGTGCCTAATGATCAAGAAATAGATGAGATG
                 ProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArgGlu
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LeuLysArgIleAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCys
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fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
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Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
                                                  carbohydrate; aromatic
                                                                                                                                                                                                   Corynebacterium glutamicum MP protein nucleotide sequence
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glutamicum
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                                   LeuThrAsnMetValThrAlaProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeu
                                                                             CTCGACAAAATTCGCAGAGCCCAGGAGCTGATTACTCGCGGCGAATCGTATGAAATCTGC
                                                                                                    LeuLysArgIleAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCys
                                                                                                                                                                                               GluAlaAlaAlaGlyPheGlyProLeuAla---ArgAlaArgHisAspLysAspAlaTyr
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industries. The polynucleotides of the invention, optionally as primers and probes, can also be used for identification and classification of C. glutamicum and related species functional or genomic mapping, functional or evolutionary studies, gene manipulation and modulation of metabolic activity. Cells containing the products of the invention may produce fine chemicals in improved yields, with higher productivity
                                                                                                                                                         polynucleotides, polypeptides and variants associated with the regulation of metabolic pathways. The products of the invention are used for production of fine chemicals, preferably amino acids and specifically lysine, but more generally nucleotides, nucleosides, lipids, fatty acid diols, carbohydrates, aromatic compounds, vitamins, co-factors and enzymes, useful in the food, animal feed, cosmetics and pharmaceutical
                                                                                                                                                                                                                                                                                                                                           microorganisms.
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                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 25; 328pp; German
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US-10-089-514-2 (1-686) x ADD13458 (1-2005)

Query Match: DB:

Best Local Percent Similarity:

Similarity:

1.76e-96 1487.00 60.06% 48.52% 41.62%

Length:
Matches:
Conservative:
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TTGAAAGCTACAGCTACCAGCGATGATGGTTTGATCATGGCATTGGCACATGAAGTGCTT
                           LeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArgHisArgGluLys
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                                                                                                                                                                           ArgAlaIleSerProValProTyrGlyAlaLeuLeuGluPheProGluLeuSerValLeu
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ATTAAAGGCACCAGGCCGCGTGGGCGAACAGCGCAAGAAGACCAAGAAATCATTGCTGAG
                     SerAlaSerProGluArgPheLeuThrIleGlyAlaAspGlyGlyValGluSerLysPro
                                                                                                                                                 CGTGGGGCCAATCCCACCGCATATGGTGCGTATCTTCAGCTGGGGGGATACCTCTATTTTG
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from

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Disclosure; SEQ ID NO

7062;

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                                                                                                                                                                                                                                                                        Nakagawa
Tateishi
                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identify mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous of the coryners.
                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000;
03-AUG-2000;
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; 2000JP-00280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 349980 BP; 79725 A; 90426 C; 98918 G; 80911 T; 0 U; 0 Other;
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                  CTGCGCACCATGGAGATCATCGATGAGCTGGAGGCAGCTCCTCGCGGTATTTACTCAGGT
                                                LysArgThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyrSerGly
                                                                                                              SerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLys
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                                                                                                             SerArgPheSerPheLeuGlyAspAspArgGlyProLeuAlaGluTyrLeuThrTyrArg
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                                                                                      CGCACGATGGAGATTATTGATGCTTTAGAGTCATCGGCTCGTGGTGTTTACTCCGGTGCG
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RESULT 11
ACF65387 1
Continuation (2 of 7
WP Sequence split in
WP Fragment Name
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WP ACF65387 2
WP ACF65387 3
WP ACF65387 3
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GCTCAGAATATATGTACTGATATCAATGAGGCTTATCTTGCAGTAGGTGGAAGACAAGAT 14550
                                                          :::::|||||||
CTCAGTAATTTCGTGCGGATAGCGGAGACGTATAAAGAGAATAATGAACAGGAAGTTACC
                                                                                                                                                 ProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArgGluIle
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                                  LeuAsnSerValCysAlaIleGlySerValHisValProArgLeuPheGluValGluThr
                                                                                                                                                         AlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleValAspLeuValArgAsnAsp
                                                                                                                                                                                                                                                       LysGlyThrArgProArgGlyGlyThrAlaGluGluAspGluArgLeuArgAlaAspLeu
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  CTTAATCAGGTATGTCGTCCAGGTAGTGTGCATGTACCTGAATTATTTAAAGTTGAGAGC
                                                                                                              AGTCAGTCTACTAAGGATAGGGCAGAAAATCTGATGATAGTGGACTTAGTGCGCCATGAT
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TyrAlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgProGlyThrSer

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                    The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duchaud E,
Buchrieser
                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                           useful e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of Photorhabdus luminescens and encoded polypeptides, e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 10240;
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TATGGCAATGATACGCATGCTTTCTGGCTTGATAGTGAAAATTCTGATAGACCCAATGCC
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CGCTTCTCAATGATGGGCAGCGGTAATGAACAAGGTGCTGTCAGACTTGAATACAGTGTA
                              ArgPheSerPheLeuGlyAspAspArgGlyProLeuAlaGluTyrLeuThrTyrArgVal
                                                                                                                                      AACCTGAATTATCGTGAATGTAAGGAGATAGTCGATCCTGAATCCTTGTTTATTCAACGT
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                ACGATGGAGATTATTGATGCTTTAGAGTCATCGGCTCGTGGTG
                                              ThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyrSerGlyAlaLeu
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The present invention describes an isolated polynucleotide (1) of CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an complement, degenerate variant or fragment; (3) a genetically engineered cc complement, degenerate variant or fragment; (3) a genetically engineered cc complement, degenerate variant or fragment; (3) a genetically engineered cc li, transfected, transformed or infected with the vector of (2); (CC 4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polypeptide that is comprised in the CC expression vector; (6) a pharmaceutical composition comprising the cc expression vector; (6) a pharmaceutical composition comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) cimmunising against Alloiococcus otitidis by administering to a host the containing the novel polynucleotide, its degenerate variant or fragment; (8) creativally engineered host cell under conditions suitable to produce the polypeptide from the culture. (1) can be used in gene therapy. The colypeptide polypeptides, antibodies and compositions of the present convention can be used for treating and diagnosing diseases, drug contening assays and monitoring of effects during and detecting Alloiococcus conventions and monitoring of effects during and detecting Alloiococcus conventions.
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18-NOV-2002; 2002US-0426742P
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The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) a expression vector comprising the novel isolated polynucleotide (I), its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic

a genetically engineered with the vector of (2); (1); (5) an immunogenic

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                                                                                             New Alloiococcus otitidis polynucleotides and polypeptides, treating and diagnosing diseases, drug screening assays and effects during drug clinical trials.
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18-NOV-2002;
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    HisGlyAlaAspSerProTyrGluLeuHisValArgArgValAspValLeuPrpAspAla
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                                                                                            LeuValArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArgLeu
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                                                                   CTCTTGCGCAATGATCTGGGCCGTTTTTGTGAAATCGGGTCGGTTGAGGTACCCCAAACTG
                                                                                                                                                      TTGATAGAAGGCCTCCGCAGTGAAGAGAAAACCAAGGCAGAAAACCTGATGATTGTCGAC
                                                                                                                                                                                            LeuArgAlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleValAsp
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Tossberg J, Wey
                           The invention relates to a method for identifying a herbicidal compound. The method of the invention comprises combining a polypeptide having at least 90% identical to any one of 48 69-1008 residue amino acid sequences (designated as p1-P48), given in the specification, with a compound to be tested for the ability to bind to the polypeptide or inhibit the activity of the polypeptide, under condictions conducive to binding or inhibiting, respectively. Also disclosed is a method for killing or inhibiting the
                                                                                                                                                                                                                                                                                                                                                      Identifying an herbicidal compound, useful for controlling undesirable vegetation, comprises combining a polypeptide with a compound to be tested for the ability to bind to the polypeptide or inhibit the activities of the activities of the ability to bind to the polypeptide or inhibit the activities that the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activiti
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      of a plant by applying to the plant the herbicidal
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bv CS, Thomas CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2760
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PheGlyArgGluIleMetAlaAsnPheArgAspLeuAlaLeuAlaHis------
                                                             ATGCATTCTTCTTCCCCCATTATGGTTTACAGTTTCATCCAGAAAGTATTGCTACCA
                                                                                                                    ArgHisArgGluLysProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAsp
                                                                                                                                                                                                                                                                                                     ACTGGGAGCCCACTTGGGAAACGGATCTGTCATTCCTGTTTCAGAAAAGTTAGAAAATCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProGlySerProAspArgGluArgAspPheGlyIleSerArgArgAlaIleThrAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTACTATTAATĠĠÁGTGĊĊŤĊĊŤĠŤĊĠŤŤATTCGGÁÁŤĠÁŤ---
                                                                                                                                                                              AGTCATTGGCCTTCGTCCCATGTTAATGGGAAACAAGATAGACACATTCTCATGGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                         ACGATTTATGATGACACTGGCTCTTTCTCTGAGAAGAATTCCTGTGTTCCTGTGAATAAC
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AspGlnGluGluGluPheThrGluThrValValLysAlaArgAlaMetValThrAlaLeu	IleValLeuAlaAspGlyGlnAlaGluPheGlyValGlyGlyAlaIleValSerLeuSer ::::::::::::::::::::::::::::::::::::	GlyAlaLeuGlyTrpPheAlaLeuSerGlyÁlaAlaAspLeuSerIleValIleArgThr ::::: :::	LysLysArgThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyrSer	ThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaPro	GluThrTyrAlaProValHisGlnLeuValŚerThrIleArgGlyArgLeuArgProGly 577 ::: 	AsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArgLeuPheGluVal AargATCTCGGTCTGTGAGCCTGGCTCAGTCCATGTACCTAACCTCATGGATGTA	AspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleValAspLeuValArg	ProlleLysGlyThrArgProArgGlyGlyThrAlaGluGluAspGluArgLeuArgAla	LeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAspGlyGlyValGluSerLys :::	AlaileSerProValProTyrGlyAlaLeuLeuGluPheProGluLeuSerVal:::	ACTCAAAACAGAAGGAAAATAGGAAATGCTGATCCTTTGGGACTTTATCTCCACCTGAGA 2067
uPheThrGlu 	pGlyGlnAla ::: AGATGAAGCT	pPheAlaLeu :: ::: \TTTCTCGTAT	tGluIleIle :: ::: TGAGATTCTC	LaCysValArc	ovalhisglr AGTACATACA	erValCysAla HGTCTGTGAC	rgGluLysasp ::: FIGAGAAGAAT	nrArgProArc	coGluArgPhe TGAAAGGTTT	11ProTyrG1) CACCATATGC	GAAAATAGG <i>I</i>
Thrvalvall:::: 	GluPheĠlyv	SerGlyÁlaA ::: RATGGTÁCGT	AspArgLeud	AlaAlaPheF GCTGCTTTCC	LeuValšerT ::: ATGGTGAGCA	IleGlyServ	ArgAlaGluð :::: CAAGCCGAGÐ	GGLYG1YThra	LeuThrIleG ;:: CTTAAGCTGG	AlaLeuLeuc CATTTCTCA	aatgctģatc
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-Q-/cgn2 1/USPTO spool h/US10089514/runat 04102005 105746 8071/app query.fasta_1.1621
-DB=18sued Patencs NA -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOODCL=0
-LOODEXT=0 -UNITS-EDite STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS-bluman40 cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US10089514 @GCN 1 116 @runat 04102005 105746 8071 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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                  Sequence 14, Appl Sequence 14, Appl Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 12, Appli Sequence 2203, App Sequence 13733, A Sequence 13713, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2
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SEQ ID NO 14
LENGTH: 2220
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APPLICANT: THIBAU
APPLICANT: BAWAS-,
APPLICANT: BLANCH
APPLICANT: COUZET
APPLICANT: BARRIE
APPLICANT: BERRIE
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Patent No. 6352839
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ALIGNMENTS

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TITLE OF INVENTION: Streptogramins And Meti
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                               APPLICANT: FAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, G
                                                                                                                                  TYPE: DNA ORGANISM: Streptomyces pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                           THIBAUT, Denis
BAMAS-JACQUES, Na
BLANCHE, Francis
COUZET, Joel
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DEBUSSCHE, Laurent
FAMECHON, Alain
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Matches:
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Gaps:
                Indels:
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APPLICANT: DUTRUC-ROSSET, Gilles
APPLICANT: DUTRUC-ROSSET, Gilles
ITITLE OF INVENTION: Streptogramins And Method For
ITITLE OF INVENTION: Streptogramins And Method For
ITITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 2220
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
ORGANISM: Streptomyces pristinaespiralis
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APPLICANT: THIBAUT, Denis
APPLICANT: BAWAS-JACQUES, I
APPLICANT: BLANCHE, Franci
APPLICANT: COUZET, Joel
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BAMAS-JACQUES, Nathalie
BLANCHE, Francis
COUZET, Joel
   GluLysProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPheGlyArg
                                  GCCGACCTGCGCGCCACCGCCCACACCGCGACGGCAGCTGATGGCCGTCGCCCACCGC
                                                                                                                                                                                      ProGluProMetHisGlyArgValSerGluValArgHisThrGlyGluAspValPheArg 118
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                                                                                                               ProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeuArgAlaIleSerProValPro
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APPLICANT: PARIS, Jean-Marc

APPLICANT: DUTRIC-ROSSET, Gilles

TITLE OF INVENTION: Streptogramins And Methoc

TITLE OF INVENTION: Mutasynthesis

FILE REFERENCE: Streptogramin genes

CURRENT APPLICATION NUMBER: US/08/765,907A

CURRENT FILING DATE: 1997-03-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6
   Percent Similarity:
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APPLICANT: THIBAUT, D
APPLICANT: BAMAS-CACQ
APPLICANT: BLANCE, F
APPLICANT: COUZET, Jo
APPLICANT: BARRIERE,
APPLICANT: DEBUSSCHE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application Patent No. 6352839 GENERAL INFORMATION:
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                                                                                                                                                    TYPE: DNA
ORGANISM: Streptomyces
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COUZET, Joel
BARRIERE, Jean-Claude
DEBUSSCHE, Laurent
FAMECHON, Alain
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BAMAS-JACQUES, Nathalie
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TyrLeuGlyTyrGluLeuLysAlaGluThrThrGlyAspProAlaHisArgSerProHis
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                                                                      ArgArgArgValProValAlaProGluLeuProPheGluPheAsnLeuGlyTyrValGly
                                                                                                                     TCAGGCGGCGAGACCCGCCGGCCCGGCACCCTCTTCGACCACCTGGAACACGAACTGGCC
                                                                                                                                           ThrThrThrArgThrArgArgPro-----PhePheAsnTyrLeuGluGluGlnLeuGlu
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRIC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEG ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 4496
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
ORGANISM: Streptomyces pristinaespiralis
                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-987-614A-6
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                              TyrLeuGlyTyrGluLeuLysAlaGluThrThrGlyAspProAlaHisArgSerProHis
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And N
TITLE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907
CURRENT APPLICATION NUMBER: US/08/765,907
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 197-03-20
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APPLICANT: THIBAUT, Denis
APPLICANT: BAMAS-JACQUES, I
APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
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                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Streptomyces
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                          LeuGluPheProGluLeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGly 489
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FAMECHON, Alain
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BAMAS-JACQUES, Nathalie
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; TYPE: DNA
; ORGANISM: Streptomyces
US-09-987-614A-1
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                                                                                                                                                    TITLE OF INVENTION: Streptogramins And Method For Preparing TITLE OF INVENTION: Mutasynthesis FILE REFERNCE: Streptogramin genes CURRENT APPLICATION NUMBER: US/09/987,614A CURRENT FILING DATE: 2001-11-15 PRIOR APPLICATION NUMBER: US/08/765,907 PRIOR APPLICATION NUMBER: US/08/765,907 PRIOR ETLING DATE: 1997-03-20 NUMBER OF SEQ ID NOS: 17
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DEBUSSCHE, Laurent
FAMECHON, Alain
PARIS, Jean-Marc
DUTRUC-ROSSET, Gilles
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Sequence 845, Application US/09902540

Patent NO. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: MYXOCOCCUS Xanthus Genome Sec.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
INVERENCE: SEQ ID NOS: 16825

SEQ ID NO 845
LENGTH: 7760
TYPE: DNA
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    ORGANISM: Myxococcus xanthus
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Sequence 8203, Application US/09902540

Patent NO. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxocoocus xanthus Genome Serille Reference: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT EILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8203
LENGTH: 1308
TYPE: DNA
ORGANISM: Myxococcus xanthus
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Best Local Similarity:
Query Match:
DB:
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               CAAATCATCACCGAGCTGGAGCCACATGCGCGCGCGCTCTATACGGGCTCGCTGGGGTAC
                                                                                                     CysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLysLysArgThrMet
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/99/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 13733

LENGTH: 1431

TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/0;
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/0;
PRIOR FILING DATE: 1998-07-27;
NUMBER OF SEQ ID NOS: 33142;
SEQ ID NO 13413
LENGTH: 1101
TYPE: DNA
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                SerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLys
                                                           AGCTATCCCAACGTGCATCACCTGGTGAGCAGCGTCACCGGCGAACTGGCGCCGGGCAAG
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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OTHER INFORMATION:
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TYPE: DNA
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1798525 CGCCGGATAGAAGAACAGGACCACGGGTCCGTCGGATAGCAGGACGCTAAGCCTGCGAGG 1798584
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                            104 GlyArgValSerGluValArgHis-----ThrGlyGluAspValPheArgGlyLeuPro
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WASSER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840Å
CURRENT APPLICATION NUMBER: US/09/103,840Å
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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                                                                                                     SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A Patent No. 6294328
               ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                            TYPE: DNA
                                                                             LENGTH: 4411529
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Oy 260 hrTyrargValAlaAspGlyValValSerValArgGlySerAspGlyThrThrArgT 280	203 yrGluLeuH18ValAtgArgValAspValLeuProAspAlaGluGluValA 22	151	104 GlyArgValSerGluValArgHisThrGlyGluAspValPheArgGlyLeuPro 12	Oy 68 ArgAlaIleThrAspSerGlyLeuProValLeuGlyValCysLeuGlyHis 84	Alignment Scores: Pred. No.: \$70.50 Score: Percent Similarity: 44.14\$ Best Local Similarity: 15.97\$ Conservative: 99 Hismatches: 285 Ouery Match: 15.97\$ US-10-089-514-2 (1-686) x US-09-103-840A-1 (1-4411529) Oy 48 IleValValSerProGlyProGlySerProAspArgGluArgAspPheGlyIleSerArg 67 ::: 1807500 GTAGTCGAAACGCCGCACCTCGGCGAATTTGGCCTGTTTCG 1807541
Db 1809156 CGCCGAAGGTGCGGGCGATGGAGCTGATCGAAGAGGTGGAAGAACACGCCGCGGGCCTTT 1809215 Qy 616 yrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIleA 636 Qy 616 yrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIleA 636	Db 1808976 GCCGAAACGACCTGGGTCGGGTCGGCTCTGCACGGCACTGTTCGGGTCGAGGATTACAGCC 1809035 Qy 556 luValGluThrTyrAlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgP 576	1808 1808	1808619 442 1808679 462 1808739	Oy 38% alArgalarroAlacthrroThrroAlamet val	1808 1808

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US-09-252-991A-811
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US-09-252-991A-811
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PRIOR ON ELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 811
LENGTH: 1506
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1525
LENGTH: 1503
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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Sequence 1525, Application US/09328352
Patent No. 6562958
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Jacques, Nathalie
Lacroix, Patricia
Thibaut, Denis
                                                                    Blanc, Veronique
Blanche, Francis
                                                   Crouzet, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 645 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
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APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Inv
TITLE OF INVENTION: Biosynthesis Of
TITLE OF INVENTION: Coding For These
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NAME/KEY:
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HYPOTHETICAL: I
ANTI-SENSE: NO
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STATE: D.C.
COUNTRY: USA
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                                   ArgLeuProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAsp
                                                                                                                                               GlyGluAlaThrGlyGlnProProValValValProAsnAsp-----AlaAspTrpSer
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1300 I Street, N.W., Suite 700
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Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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CGGATGCTCGCCAACTTCCGCGACCTGTCCCTG
                         GluIleMetAlaAsnPheArgAspLeuAlaLeu 189
                                                                  CACCTGCCCCGCTTCGGCGTGCAGTTCCACCCCGAATCGATCAGCAGCGAACACGGCCAC
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Search completed: October 5, 2005, 21:02:45
Job time: 6032.42 secs

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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool h/US10089514/runat_04102005_105745_8055/app_query.fasta_1.1621
-DB=PublIshed_ApplicatIons_NA -QFWT=fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10089514 @CGN 1 1 920 @runat 04102005_105745_8055
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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GENERAL INFORMATION:

APPLICANT: YANAI, KOJİ

APPLICANT: SUMIDA, Naomi

APPLICANT: WATANABE, Manabu

APPLICANT: WATANABE, Manabu

APPLICANT: MORIYA, Tatsuki

APPLICANT: MURAKAMI, Takeshi

TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods for INVENTION: Producing The Same And Novel Biosynthesis Genes

FILE REFERENCE: 2003-1302A/WMC/00144

CURRENT APPLICATION NUMBER: 80227/2001

PRIOR APPLICATION NUMBER: 82227/2001

US-10-472-587-1

ALIGNMENTS

Sequence 1, Application US/10472587 Publication No. US20040214274A1

Pred. No.

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; TYPE: DNA; CORGANISM: Streptomyces v; FEATURE; ; FEATURE; ; NAME,KEY: CDS; LOCATION: (1)...(2058) US-10-472-587-1
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                               SerProTyrGluLeuHisValArgArgValAspValLeuProAspAlaGluGluValArg
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61 ArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeuGlyVal 8	Qy 41 ProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArgGlu 60 :::	Qy 21 GlyGluAlaThrGlyGlnProProValValValProAsnAspAlaAspTrpSerArgLeu 40	Qy 1 MetArgThrLeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIle 20	.089-514-2 (1-686) x US-10-126-927-68 (1-3305)	Hest Local Similarity: 90.99% Mimatches: 42 Query Match: 87.53% Indels: 17 DB: 14 Gaps: 3	No.: 1.3e-301 Length: 3127.50 Matches: Conservative:	US-10-126-927-68 Alignment Scores:	LENGTH: 3305 TYPE: DNA	SOFTWARE: PatentIn ver		FILE REFERENCE: 54-000120US CURRENT APPLICATION NUMBER: US/10/126,927 CURRENT FILING DATE: 2002-04-19 PRIOR APPLICATION NUMBER: US 60/285,030	; APPLICANT: Pastrnak, Miro ; APPLICANT: Santoro, Stephen W ; APPLICANT: Santoro, Stephen W ; APPLICANT: Zhang, Zhiwen ; TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids	; APPLICANT: Liu, David R ; APPLICANT: Magliery, Thomas ; APPLICANT: Meggers, Eric L ; APPLICANT: Mehl, Ryan A	; APPLICANT: Wang, Lei ; APPLICANT: Anderson, John C ; APPLICANT: Chin, Jason	PUBLICATION NO. US2003008257 GENERAL INFORMATION: APPLICANT: The Scripps Rese	(n h	2041	Qy 681 AlaValAlaGlyAlaArg 686	1981 GAGGAGTTCACCGAGACCGTGGTAAAGGCCCGCGCCATGGTCACCGCCCTCGACGGCAGC	661		Qy 621 GlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIleArgThrIleValLeu 640
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Sequence 67, Application US/10126927
Publication No. US20030082575A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Liu, David R
APPLICANT: Liu, David R
APPLICANT: Meggers, Eric L
APPLICANT: Meggers, Eric L
APPLICANT: Mestrnak, Miro
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Shang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
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PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VEYSION 3.1
SEQ ID NO 67
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US-10-126-927-67
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CCCATGGAGATCATCGACCGCCTGGAGGAAGGCCCCCGGGGCGTCTTACCCGGGGCGCTC
                       ThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyrSerGlyAlaLeu
                                                                                              AlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLysLysArg
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GTCTGCCTGGGCCACCAGGGCATGGCCCTCGCCCACGGCGCCCGGGTGGGCCCGGGCCCCC
              ValCysLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAlaPro
                                                  CCGGCCGACTTCGGCCTGTGCGCCCGGATCGCCGAGGAGGGCCGGCTGCCCGGTGCTCGGC
                                                               GluArgAspPheGlyI1eSerArgArgAlaI1eThrAspSerGlyLeuProValLeuGly
                                                                                                  MetArgThrLeuLeuIleAspAsnTyrAsp$erPheThrHisAsnLeuPheGlnTyrIle
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            GlyGluSerTyrGluIleCysLeuThrAsnMetValThrAlaProThrGluAlaThrAla
                                                                                    ArgHisAspLysAspAlaTyrLeuLysArgIleAspGluCysLeuLysGluIleArgAsn
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                                                                                                                                                                                            AlaMetValPheGlyIleProGluAla---AlaAlaGlyPheGlyProLeuAlaArgAla
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1167
                                                                                                                                                                                                                                                    Sequence 1167, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: IXEDA, HARUO
APPLICANT: HARIKAWA, JUN
APPLICANT: HARIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HARTORI. MASAHIRA
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672 AlaMetValThrAlaLeuAsp 678
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                                                              GCCGTCATCGCGCTCTCCGACCCGGCCGACCGAGTTCGAGGAGACGGCGGTCAAGGCCCGCC 20658
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; ORGANISM: Streptomyces a
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; LOCATION: (1)...(2196)
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Best Local Similarity:
Query Match:
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; LOCATION: (4187715)
; OTHER INFORMATION: a, 1
US-10-156-761-1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
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SEQ ID NO 1
LENGTH: 9025608
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                               Sequence 1111, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                 APPLICANT:
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DB:
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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LENGTH: 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/494,675
CURRENT FILLING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: PCT/EP02/12141
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 101 54 292.1
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2011-11-05
NUMBER OF SEQ ID NOS: 164
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APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: Genes coding
FILE REFERENCE: BGI-163US
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APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Kroger, Burkhard
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEJIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09738626 Publication No. US20020197605A1
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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GlyAlaSerArgFheSerFheLeuGlyAspAspArgGlyProLeuAlaGluTyrLeuThr
                                                    GAAACATTCTTTGCCCATTCCTCCCATGCTTTTTTGGCTCGATGAT---
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 CTGCGCACCATGGAGATCATCGATGAGCTGGAGGCAGCTCCTCGCGGTATTTACTCAGGT
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APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: MCMICHAEL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCO
FILE REFERENCE: AM100780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/4333,777
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 2046
TYPE: DNA
ORGANISM: Alloiococcus otitidis
FEATURE:
NAME/KEY: CDS
LOCATION: (22)...(2043)
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APPLICANT: CMCHICLEL, JOHN CALHOUN
APPLICANT: CMCHICLEL, JOHN CALHOUN
APPLICANT: CMCHICLEL, JOHN CALHOUN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: DOLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THERE
FILE REFERENCE; AMNOTABE: US/10/501,282
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-25
PRIOR APPLICATION NUMBER: FCT/US02/36123
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
SEQ ID NO 6651
LENGTH 1754382
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 6651, Application US/10501282 Publication No. US20050203280A1 GENERAL INFORMATION:
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SerLeuSerAspGlnGluGluPheThrGluThrValValLysAlaArgAlaMetVal
                                                                                                                                         ATCTATTCTGGGACTATTGGCTTTTTAGCCAACAATTCCACTATAGACTTCAACATCGTC
                                                                                                                                                                                 ValTyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleVal
                                                                                                                                                                                                                                                                      GlyAlaProLysLysArgThrMetGluIleIleAspArgLeuGluGluGluGlyProArgGly
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                                                 ATCCGGACCAGTGTGGTGGAAGCAGCAAGCATCGGCCTGGGGGGTGCGATTGTC
                                                                                                                                                                                                                                          GGGCGCCTAAAAAAAGAACCCTGGAAATTATTGATGACTTAGAAGCAGTTCCCAGAGGG
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                                                                                            IleArgThrIleValLeuAlaAspGlyGlnAlaGluPheGlyValGlyGlyAlaIleVal
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DB:
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Best Local Similarity:
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, ping
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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LOCATION: (1)..(3023)
OTHER INFORMATION: unsure at
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113 GlyGluAspValPheArgGlyLeuPro-----SerProPheThrAlaValArg 128
                                                                                                                                                                         74 Gly---LeuProValLeuGlyValCysLeuGlyHisGlnGlyIleAlaGlnLeuPheGly 92
                                                                                                                                                                                                                                                                      54 ProGlySerProAspArgGluArgAspPheGlyIleSerArgArgAlaIleThrAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyGluAlaThrGlyGlnProProValValValProAsnAspAlaAspTrpSerArgLeu
                                               GCTAAAATCGTCCATGCTCCAAGCTATACATGGCCGGCTTAGTGAACTTGAACACAAT 2526
                                                                                                                                           GGAGATATACCCATCCTGGGTGTCTGCCTTGGCCACCAGGCCCTGGGATTTGTCCATGGT
                                                                                         GlyThrValGlyLeuAlaProGluProMetHisGlyArgValSerGluValArgHisThr 112
                                                                                                                                                                                                                                          CCGGGATCTCCGGCCTGCCCTAGCGACATAGGTATAGGCCTGCGGATACTTTGCGAGTGT
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Wu, Wei
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Matches: Conservative: Mismatches:

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3537
LENGTH: 3023
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3537, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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AlaLeuAspHisGlnGluGlyCysCysTyrLeuLeuAlaLeuAspArgArg 362	ب ى ب	307 PheAsnLeuGlyTyrValGlyTyrLeuGlyTyrGluLeuLysAlaGluThrThrGly 325	289 GluGluGlnLeuGluArgArgArgValProValAlaProGluLeuProPheGlu 30 ::::::::::::::::::::::::::::::::::::	ArgGlySerAspGlyThrThrArgThrArgArgProPhePheAsnTyrLeu 288 	257 GluTyrLeuThrTyrArgValAlalaspGlyValValSerVal :::: :::	SerValLeuGluGlyAlaSerArgPheSerPheLeuGlyAspAspAsgGlyProLeuAla 256	217 GluGluValArgArgGlyCysLeuProGlyGluGlyThrThrPheTrpLeuAspSerSer 236 ::: 	212ProAspAla 216 	196ArgHisGlyAlaAspSerProTyrGluLeuHisValArgArgValAsp 211 	191 His	189Leuala 190 2105 CAGACACCATTGCTTCAGGAAAGAAGAACATTCTCCAGATCTCAAGAACTTTGTTGCA 2046	174 SerAspPheGlyArgGluIleMetAlaAsnPheArgAspLeuAla 188 	GlyLeuArgHisArgGluLysProLeuTrpGlyValGlnPheHisProGluSerIleGly 1	149ValValMet 153	148 148 2345 ACCTTGTGGGGATCATTGGATAACTTATTCGTAACAAACCAGTCAGAGTGCAGTACCACT 2286	147 148 2405 ACTGCTTCTCCAAAAATGCTCTCATTCCTTGAAAGCGATAAGCCTGATATAACTAGCAGT 2346	129 TyrHisSerLeuAlaAlaThrAspLeuProAspGluLeuGluProLeuAlaTrp 146	::: :::
RESULT 13 US-10-282-122A-17825 ; Sequence 17825, Application US/10282122A	Qy 657 SerAspGlnGluGluPheThrGluThrValValLysAlaArgAla 672	37 ThrileValLeuAlaAspGlyGlnAlaGluPheGlyValGlyGlyAlaI :::	Qy 617 SerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIleArg 636 :::: ::: ::: ::: :::	Qy 597 ProLysLysArgThrMetGluIleIleAspArgLeuGluGluGlyProArgGlyValTyr 616	Qy 577 GlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGlyAla 596	Qy 557 ValGluThrTyrAlaProValHisGlnLeuValSerThrIleArgGlyArgLeuArgPro 576 :: :: ::	Qy 537 ArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArgLeuPheGlu 556	AlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleValAspLeuVal 53	Db 1017 1017	1037 ATATGTTGCTCTTGAA	459 Arc 1097 CGA	440 ThrasnMetValThrAlaProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeu	Qy 420 LysArgIleAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCysLeu 439	Qy 400 GluAlaAlaAlaGlyPheGlyProLeuAlaArgAlaArgHisAspLySAspAlaTyrLeu 419		377 GluThrLeuThrGlyLeuAlaValArgAlaPro	363 GlyHisAspAspGly	1478 GTGGTTGATCACAACAATGGGGATGTGTACATTTATCATTACATGATGATGATATTCTTCT

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; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-17825
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION UMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/267,636
PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - NUMBER OF SEO ID NOS: 78614
SOPTWARE: Patentin version 3.1
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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FILING DATE: 2000-09-06
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                     GCAGAAGACGTCGGCATAAGCGCGTGGGTATTACAAACAGCACAGTGCCCAGTGCTGGGC
                                           GluArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeuGly 79
                                                                                                                                                             GGGGCCCGCACCCACGTGGTCACCAACAACGTATCCCCAGAGGACATTGATCTAGACCGC
                                                                                                                                                                                          ThrGlyGlnProProValValVal------ProAsnAspAlaAspTrpSerArg 39
                                                                                                                                                                                                                                                                  LeuLeuIleAspAsnTyrAspSerPheThrHisAsnLeuPheGlnTyrIleGlyGluAla
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
                                                                                                             LeuProValGluAspPheAspAlaIleValValSerProGlyProGlySerProAspArg 59
                                                                                                                                                                                                                               TIGGIGGIGGATAATTICGATTCCTTCACCTACAACATCGTCGACTACCTCCACCGCTGC 78
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                                    GTACGCGACTCCCGAGAACGCTACATGGCTACGATCGAGCGGATCCAAGAAGCGATTCGA
                                                                   AlaArgHisAspLysAspAlaTyrLeuLysArgIleAspGluCysLeuLysGluIleArg
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                                                                                                        GTGCCCACGGTGCCGAGTTTCAACCCG-----ACTGGTATCGGGCGGTTG---CAC
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RESULT 14
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                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Wang, Li
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TITLE OF INVENTION: Identification of Essei
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                       Yamamoto, Rol
Forsyth, R.
Xu, H.
                                                                                                                       Trawic.
Carr, Grant
Carr, Grant
Robert
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Malone, Cheryl
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-02-09
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OR APPLICATION NUMBER: 60/206,848

OR FILING DATE: 2000-05-23

OR APPLICATION NUMBER: 60/207,727

OR FILING DATE: 2000-05-26

OR APPLICATION NUMBER: 60/230,335

OR APPLICATION NUMBER: 60/230,337

OR APPLICATION NUMBER: 60/230,347

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OR APPLICATION NUMBER: 60/230,347

OR FILING DATE: 2000-09-09
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FILING DATE: 2000-10-23
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                           LeuArgHisArgGluLysProLeuTrpGlyValGlnPheHisProGluSerIleGlySer
                                                                         AATACAGTTCCAAAAGAATTAGAAATTACAGCAATTACTGATAAAGGGGAAATAATGGGG
                                                                                               ThrAspLeuProAspGluLeuGluProLeuAlaTrpSerAspAspGlyValWetGly
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APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Literal innocua, genôme and
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
VOUNBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
FENCETH. GRATO7
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; Sequence 9, Application US/10398221
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TYPE: DNA
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LOCATION: (1)..(end)
OTHER INFORMATION: n ca
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374902		374902
374	ys T yr LeuLeuAlaLeuAspArgArgGlyHisAspAspGlyAlaArgAlaTrpLeuArgG	354
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354	rgAlaIleAlaLeuAspHisGlnGluGlyCysC	334
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216	HisGlyAlaAspSerProTyrGluLeuHisValArgArgValAspValLeuProAspAla	197
196 375108	GlyArgGluIleMetAlaAsnPheArgAspLeuAlaLeuAlaHisHisArgAlaArgArg	177 375131
176 375132	HisargGluLysProLeuTrpGlyValGlnPheHisProGluSerIleGlySerAspPhe	157 375191
156 375192	LeuProAspGluLeuGluProLeuAlaTrpSerAspAspGlyValValMetGlyLeuArg ::: :::	137 375251
136 375252	GlyLeuProSerProPheThrAlaValArgTyrHisSerLeuAlaAlaThrAsp	119 375311
118 375312	ProGluProMetHisGlyArgValSerGluValArgHisThrGlyGluAspValPheArg	99 375371
98 375372	GlyValCysLeuGlyHisGlnGlyIleAlaGlnLeuPheGlyGlyThrValGlyLeuAla	79 375431
78 375432	ArgGluArgAspPheGlyIleSerArgArgAlaIleThrAspSerGlyLeuProValLeu 	59 375482
58 375483	AspPheAspAlaIleValValSerProGlyProGlySerProAsp	44 375542
43 375543	ThrGlyGlnProProValValValProAsnAspAlaAspTrpSerArgLeuProValGlu	24 375587

664 hrGluThrValValLysAlaArgAlaMetValThrAlaLeuAspGlySerAlaVal 682 	Qy 6 Db 3740
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624 laLeuSerGlyAlaAlaAspLeuSerIleValIleArgThrIleValLeuAlaAspGlyG 644 	Qy 6 Db 3741
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584 alArgAlaAlaPheProGlyGlySerMetThrGlyAlaProLy8Ly8ArgThrMetGluI 604 	Qy 5 Db 3742
564 isGlnLeuValSerThrIleArgGlyArgLeuArgProGlyThrSerThrAlaAlaCysV 584 ::: ::: ::: :::	Qy 5 Db 3743
544 ysAlaIleGlySerValHisValProArgLeùDheGluValGluThrTyrAlaProValH 564 	Qy 5 Db 3743
524 ysAspArgAlaGluAsnLeuMetIleValAspLeuValArgAsnAspLeuAsnSerValC 544 ::: :::	Qy 5 Db 3744
504 roargGlyGlyThralaGluGluaspGluArgLeuArgAlaAspLeuAlaGlyArgGluL 524	Qy 5 Db 3745
484 rgPheLeuThrIleGlyAlaAspGlyGlyValGluSerLysProIleLysGlyThrArgP 504	Qy 4 Db 3745
464 alProTyrGlyAlaLeuLeuGluPheProGlüLeuSerValLeuSerAlaSerProGlüA 484	Qy 4 Db 3746
446ProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeuArgAlaIleSerProV 464	Qy 4 Db 3746
426 euLysGluIleArgAsnGlyGluSerTyrGluIleCysLeuThrAsnMetValThrAla- 445 	Qy 4 Db 3747
407 roLeuAlaArgAlaArgHisAspLysAspAlaTyrLeuLysArgIleAspGluCysL 426	Qy 4 Db 3748
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Search completed: October 6, 2005, 00:28:12 Job time: 20108.7 secs

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-DB=EST -OFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPECH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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ALIGNMENTS

sinensis L. Ösbeck) seedling Unpublished (2003) Contact: Michael Bausher Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en rosids; eurosids II; Sapindales; Rutaceae; Citrus. BQ625203.1 GI:21652372 EST. 2001 South Rock Rd., Fort Pierce, Tel: (772) 462-5918 US Horticultural Research Expressed sequence tags isolated from entire sweet orange (C 1 (bases 1 to 698)
Bausher, M., McKendree, W., Dang, P., Chaparro, J., Email: mbausher@ushrl.ars.usda /organism="Citrus sinensis" /mol_type="mRNA" /cultivar="Ridge Pineapple" /db_xref="taxon:2711" Location/Qualifiers pineapple sweet orange USDA-FP_02294 5', mRNA dq 869 FL 34945, mRNA linear EST 01-JUL-20 entire seedling Citrus sequence. USA Shatters, R., a; Tracheophyta; eudicots;

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RESULT 2
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COO24641 894 bp mRNA linear EST 10-JUN-2004 ESTB03025 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb Coccidioides posadasii cDNA clone CIFA227 3' end, mRNA sequence. CO024641 GI:48551893 EST. Coccidioides posadasii
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/tissue_type="entire seedling"
/dev_stage="50 days after germination"
/lab_host="XL1-Blue"
/clone_lib="Ridge pineapple sweet orange entire seedling"
/clone_lib="Ridge pineapple II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; A high quality EST with at least 200 contiguous
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Tel: 301 838 3519
Fax: 301 838 0208
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1 (bases 1 to 894)

Gardner, M.J. and Cole, G.T.

Analysis of gene expression in Coccidioides posadasii mycelia spherules via expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Other_ESTs: EST803026
Contact: Gardner MJ
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                                                                        TCTCCATCAAAATCAATCAAGGTCCCGAAAACTACTCCACGTTGAAAGCTACGAAACAGTA
                                  CysAlaIleGlySerValHisValProArgLeuPheGluValGluThrTyrAlaProVal
                                                                                                                                                      GCCGTCAGCCCAGACAAAGAAGAAGACGAGCGGAGAAAAAGTCAGTTAGCGACGGATGTC
                                                                                                                                                                                    ProArgGlyGlyThrAlaGluGluAspGluArgLeuArgAlaAspLeuAlaGlyArgGlu
                                                                                                                                                                                                                                                      ArgPheLeuThrIleGlyAlaAspGlyGlyValGluSerLysProIleLysGlyThrArg
                                                                                                                                                                                                                                                                                                                                              TyrGlyAlaLeuLeuGluPhe-----ProGluLeuSerValLeuSerAlaSerProGlu
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pExpress 1; Site 1: Not I; Site 2: Coccidioides posadasii spherule cDNA library, 0.5 kb "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="spherules"
/lab_host="E. coli DH10B,
/clone_lib="Coccidioides
0.5 to 5.3 kb"
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/db_xref="taxon:199306"
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                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                  Other ESTs: A1940862 corresponding to Gm-c1010-1280 (5') Contact: Vodkin, L.O., PI, A Functional Genomics Program Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. an A. Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                    Genomics
University of Illinois
Edwin R. Madigan Building,
Tel: (217) 244-6147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 859)
                                                                                                                                                                                                                                                                                                                                       (217) 244-6147
(217) 333-4582
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                                                                                                           /organism="Glycine max"
/mol type="mRNA"
/db xref="taxon:3847"
/clone="Gm-r1070-1549"
/clone_lib="Gm-r1070"
/clone_lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,98 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or
                                                                                                                                                                                                                                                                                                                                       333-4582
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   197 ACAAGGGCTGTG 186
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a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.bc.umm.edu/ResearchProjects/Soybean/index.html. Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under

red. No.: core: core: srcent Similarity: sst Local Similarity: tery Match:	4.42e-43 Length: 859 567.00 Matches: 113 imilarity: 72.55% Conservative: 35 L Similarity: 55.39% Mismatches: 56 h: 15.87% Indels: 0 Gaps: 0	
3-10-089-514-	114-2 (1-686) x BE658136 (1-859)	
, 474 5 797	174 GluLeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAspGlyGly 493	
737	94 ValGluSerLy8BroIleLy8GlyThrArgProArgGlyGlyThrAlaGluGluAspGlu 513 	
, 514	14 ArgLeuArgAlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleVal 533	
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534 617	34 AspLeuValArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArg 553	
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574	774 LeuArgProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMet 593	
594		
437	37 ACAGGTGCANNTAAGTTGAGATCAATGGAACTTCTTGATTCTATTGAAAGTTGTTCTCGA 378	
, 614 , 377	14 GlyValTyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIle 633	
634	34 ValileArgThrIleValLeuAlaAspGlyĠlnAlaGluPheGlyValGlyGlyAlaIle 653	
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257		
674	74 ValThrAlaLeu 677	

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vodkin, L., Shoemaker, R., Keim, P., Polacco, J.C., Retzel, E., Khanna, A., Shealy, R., Clough, S., Thibaud-Nissen, F., Coryell, V., Erpelding, J., Gonzalez, D.O., Stromvik, M., Rodriguez-Huete, A.M.,
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CO980064.1 GI:51336198
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Plate: GM89007A1 row: C
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Tel: (217) 244-6147
Fax: (217) 333-4582
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h quality sequence stop: 768.
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                                                                                                                                                                                                                                                                                                                                                            from young leaves or hypocotyls exposed to bacterial and fungal pathogens (source libraries Gm-c1072, Gm-c1073, Gm-c1074) and G63 from roots of young plants grown in hydroponic media without phosphate (source library Gm-c1087). The 5' RSTs of the source clones from the different libraries were used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1089 and the cDNA clones of the reracked Gm-r1089 library were then sequenced at the 3' end. The unigene selection and 3' sequencing was funded by NSF plant Genome project #9872555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from germinating cotyledons(source library Gm-c1069, Gm-c1076, and Gm-c1077); 1.465 cDNAs from various tissue and organ systems of the adult plant; 476 cDNAs from adult stem tissue (source library Gm-c1062); 1340 cDNAs from tissue culture derived somatic embryos (source libraries Gm-c1036 and Gm-c1075); 2918 cDNAs from hypocotyls or young seedlings; 742 cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1065, Gm-c1066, and Gm-c1068); 839 cDNAs from control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control of the process of the control 
(http://soybeangenomics.cropsci.uiuc.edu/) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vodkin, University of the Northern Arizona State University, and Paul Keim, Northern Arizona University as part of the Public EST project, http://129.186.26.94/soybeanest.html. The contig analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 different cDNA libraries constructed from various tissues and stages of development of soybean including 973 cDNAs
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/clone_lib="Gm-r1089"
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/note="The library Gm-r1089 is a sequence-driven, re
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corresponding 5' EST from each clone in the Gm-r1089 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the clone ID of the original cDNA library that is also listed under 'OTHER EST'." sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The to select unique genes was performed by the laboratory Ernest Retzel. Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3 Of.

8 밁 Ś 뫄 Š 밁 Ş Вþ Ş 밁 S 밁 S 맖 Š 밁 Ś Ş 맑 밁 밁 US-10-089-514-2 (1-686) x CO980064 (1-768) Query Match: Best Local Score: Alignment Scores: Percent Similarity: No. 325 505 654 ValSerLeuSerAspGlnGluGluGluPheThrGluThrValValLysAlaArgAlaMet 673 594 445 AAGCGGTCAGATGTCAGTGCTGTAGACTGTGTCAAAGCTGCATTTCCTGGTGGTTCAATG 574 LeuArgProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMet 554 534 AspLeuValArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArg 514 ArgLeuArgAlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleVal 494 ValGluSerLysProIleLysGlyThrArgProArgGlyGlyThrAlaGluGluAspGlu 745 GATCTGAGTATTTGCTGTTCTTNNNNTGAGAGGTTCCTGCAGNNNGATAGGAAGAATATA 686 474 GluLeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAspGlyGly 493 Similarity: ValIleArgThrIleValLeuAlaAspGlyGlnAlaGluPheGlyValGlyGlyAlaIle LeuPheGluValGluThrTyrAlaProValHisGlnLeuValSerThrIleArgGlyArg ValThrAlaLeu 677 GTTGCTCTGTCAAACCCTGAAGACGAGTATGAAGAGATGGTTTTGAAGACAAAAGCCCCCA 146 GTGATAAGAACAGTCATTGTACACGAGGGTGAAGCTTCAATAGGAGCTGGAGGGGCAATT GGTATCTÁCTCÁGGCTGTATTGGÁTTTŤŤCTCATATAATCAAGCÁTTTGÁŤCTÁAATÁŤŤ GlyValTyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIle ACAGGTGCACCTAAGTTGAGATCAATGGAACTTCTTGATTCTATTGAAAGTTGTTCTCGA ThrGlyAlaProLysLysArgThrMetGluIleIleAspArgLeuGluGluGlyProArg CTCATGGATGTGGAATCATATGCAACTGTTCACACAATGGTGAGTACTATTCGTGGGAAG GACCTTCTAAGGAATGACCTTGGCCGTGTTTTTGATCCTGGATCTGTTCATGTGCCACGT CAACTAAAATTTAAATTACAGTTCAGCGAAAAGGATCAGGCTGAAAACCTGATGATTGTT CTAGAAGCTAAGCCCATCAAGGGAACGATAGCTCGTGGTGCTACTGAAGAGGAAGATGAG 4.66e-43 566.00 73.04% 55.39% 15.84% Mismatches: Indels: Matches: Conservative: Gaps: 768 113 36 55 653 326 593 573 533 513 206 266 633 613 386 446 506 553 626

RESULT 5 CO030342/c

DEFINITION TOCUS

CO030342
818 bp mRNA linear EST 10-JUN-200
EST808726 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone CIFB368 3' end, mRNA sequence

EST 10-JUN-2004 ary, 0.5 to 5.3

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REFERENCE
AUTHORS
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VERSION
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Best Local Similarity:
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Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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Unpublished (2003)
Other EST8: EST808727
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Gardner, M.J. and Cole, G.T.
Gardner, M.J. and Cole, G.T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Gardner MJ
The Institute for Genomic Research
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CO030342.1
                                                                                                AlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeuMetIleValAspLeuVal
                                                                                                                                                              ValLeuSerAlaSerProGluArgPheLeuThrIleGlyAlaAspGlyGlyValGluSer 496
                                                                                                                                                                                                                                                                                                                                                                                           CAGAAGATCCGGGCCGCACAGAATGCCATTAAGGAGGCGAGGCGTATGAGGTGACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                 LysArgIleAspGluCysLeuLysGluIleArgAsnGlyGluSerTyrGluIleCysLeu
                                                                                                                                          AAACCAATAAAGGGAACCCTTGCCGTCAGCCCAGACAAGAAGAAGAAGACGAGCGGAGAAAA
                                                                                                                                                                                                    ATACTCTCTTCGTCGCCCGAGAGGTTTATATCCATAGATGCTGATGGCGTGGCTGAAATG
                                                                                                                                                                                                                                                                  CGAGAACGTAACCCCGCCCTTACTCAGCGTATATAGACTTCCGTGTCAACGAGACCACC
                                                                                                                                                                                                                                                                                               ArgAlaIleSerProValProTyrGlyAlaLeuLeuGluPhe-----ProGluLeuSer 476
                                                                                                                                                                                                                                                                                                                               ACGACAAAATTCAAGGCATCGTGTCCGGATGTAGACCCATACGCATTATATCTCTCCCTT
                                                                                                                                                                                                                                                                                                                                                            ThrAsnMetValThrAlaPro---ThrGluAlaThrAlaLeuProLeuTyrSerAlaLeu
                 ArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArgLeuPheGlu
                                                                               AGTCAGTTAGCGACGGATGTCAAGGAGCTCGCCGAGAACTTAATGATTGTCGATCTTATC
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coccidioides posadasii spherule cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="spheriles"
/lab_host="E. coli DH10B, T1 phage
/clone lib="Coccidioides posadasii
0.5 to_5.3 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol
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/clone="CIFB368"
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62.98%
46.95%
15.73%
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Indels:
Gaps:
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Conservative:
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Percent Similarity:
Best Local Similarity:
                                 Score:
                                                             Alignment
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REFERENCE
AUTHORS
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ORGANISM
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CO034510/c
LOCUS
ORIGIN
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Coccidioides posadasii
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EST812894 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone CIFBU13 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_ESTs: EST812895
                                                                                                                                                                                                                                                                                                                                                                                                            Analysis of gene expression in Coccidioides spherules via expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 820)
Gardner, M.J. and Cole, G.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pežizomycotina; Eu
Onygenales; mitosporic Onygenales; Coccidioides.
                                                                                                                                                                                                                                                 Email: gardner@tigr.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     The Institute for Genomic 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                          Contact: Gardner MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C0034510.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleValIle 635
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                  /note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV.
Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb "
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                                                                  /dev_stage="spherules"
/lab_host="E. coli DH10B, Tl phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
/.5 to_5.3 kb"
                                                                                                                                         /db_xref="taxon:199306"
/clone="CIFBU13"
                                                                                                                                                                          organism="Coccidioides"
/mol_type="mRNA"
/strain="C735"
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No. :

1.53e-42 561.00 64.03% 48.22%

Length: Matches: Conservative: Mismatches:

820 122 40 87

Scores:

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RESULT 7
CG942457
LOCUS
 REFERENCE
AUTHORS
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VERSION
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                                                                                    ORGANISM
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                        survey sequence.

G942457

CG942457.1 GI:39847070

GSS.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tra

Eukaryota, Magnoliophyta, eudicotyledons, core eudi

Spermatophyta, Magnoliophyta, Fabaceae, Papilionoideae,
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 Town, C.
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                                                                                                                                                                                                                                                                                                                                                         GCCAGCGGCACCGTCGATCAGTCGGTGGTTATCCGTACGATTGTAAAGTACGGAAAGCAG
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(bases 1 wn, C.D., S
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 Shetty, J.,
              to 893)
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Seq primer: TGTAAAACGACGGCCAGT
Class: BAC ends
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Unpublished (2003)
Other_GSSs: MBEHO90TR
Contact: Chris Town
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             CGAACTGTCTCGTTTTTCTTTTCAGTGAAAAGGATCAGGCAGAAAACCTGATGATTGTT
                                                                    TAACTTACTACATTTTTTGTCATGACATCAAATTTCCAAGCAACTGATTGAAATCTGTTG
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/note="Vector: pBeloBAC11; Site_1: HindIII; Si/
/note="Vector: pBeloBAC11; Site_1: HindIII; Si/
HindIII; Cook, D.R. and Kim, D.J, unpublished"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago trun
/mol_type="genomic DNA"
/cultivar="genotype A17"
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/clone="57P11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: stein@ipk-gatersleben.de
Insert Length: 529 Std Error:
Plate: 15 row: I column: 14
Seg primer: Ml3rev.
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Tel: 039482-5522
Fax: 039482-5595
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Institute of Plant Genetics and Crop Plant Research
Corrensstr. 3, 06466, Gatersleben, Germany
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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HS15I14r HS Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare subsp. vn/mol type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="caxon:112509"
/clone="HS15114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Potokina, E., Michalek, W., Weschke, W.,
                                                               /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sali,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                        /tissue_type="embryo + scutellum"
/dev stage="0-16 hours after imbibition"
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                                                                                                                                             l (bases 1 to 620)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Romning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
Glovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW223881
EST300692 tomato
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                                                                                                            Clemson University
                                                                                                                            Clemson University Genomics Institute
                                                                     Email: http://www.genome.clemson.edu/orders/index.html
                                                                                         100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                               AW223881.1 GI:6535565
                                                      prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTCAGACCCGGAGGCGGAGTACGCCGAGATGATGCTCAAGGCG
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                                                      sequence
                                  Location/Qualifiers
organism="Lycopersicon esculentum'
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76.00%
62.29%
15.48%
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Best Local
Query Match
DB:
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TACTCGGGCTGCATTGGA
                                                                                 GCACCAAAGTTGAGATCAATGGAACTTCTTGATCATCTTGAAAATTGTTCGAGGGGCATA
                                                                                                                                                                     TCAGATGCAAGTGCAATTGATTGTGTTAGAGCTGCATTCCCTGGTGGGTCAATGACAGGT
                                                                                                                                                                                           ProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThrGly
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                                       TyrSerGlyAlaLeuGly 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pericarp"
/dev_stage="red_ripe (7-20 days_post-breaker)"
/dev_stage="red_ripe (7-20 days_post-breaker)"
/clone_lib="tomato_fruit_red_ripe, TAMU"
/note="Vector: pBlueScript_SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni; Fruit_were_tagged_at_the
breaker stage (first_sign_of_lycopene_accumulation_on_the
blossom end_of_the fruit) and harvested 7 days
post-breaker (fully_red-ripe), 10 days_post_breaker, and
20 days_post_breaker (over-ripe). 20 day fruit_which
showed_external_or_internal_signs_of_pathogenesis_were
discarded. Fruit_were_cut_in_half_and_the_seeds_and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="TA496"
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547.50
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AUTHORS
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Best Local Similari
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                             511 GluAspGluArgLeuArgAlaAspLeuAlaGlyArgGluLysAspArgAlaGluAsnLeu
                                                                                                     491
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                                                                                                                                                                     473 ProGlu-----LeuSerValLeuSerAlaSerProGluArgPheLeuThrIleGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (850) 412-7393, (772) 462-5898
Fax: (850) 561-2617, (772) 462-5886
Email: jiang.lu@famu.edu, hong.huang@famu.edu,
whunter@ushrl.ars.usda.gov, pdang@ushrl.ars.usda.
Seq primer: T3 Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Jiang Lu, Wayne Hunter, Phat
Genetic Lab, Viticulture Center; U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 645)
Hunter, W.B., Dang, P.M., Chaparro, J.X., Lu,
Genes expressed in Vitis shuttleworthii L
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vitis shuttleworthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CV099881 645 bp mRNA linear EST FAMU_USDA_FP_7904 Vitis shuttleworthii L., grape Vitis shuttleworthii cDNA clone WHVs046_D11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tallahassee, FL; Ft. Pierce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMU, USDA-ARS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vitis shuttleworthii
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GAAGATGAACACCTCAAATTGCAACTACAATACAGTGAAAAAGATCAGGCTGAAAATCTG
                                                                                        GGACTTTATCTTAACCTTAGAGAAAAAAATCCAGCACCATATGCAGCCTGGCTTAATTTT
                                                                                                                                                                                                                                                                                      AGTTATGAATTGTGTCTTACAACTCAAATGAGAAAGAGAATTGGGCAAATAGATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:246827"
/clone="MHV8046 D11"
/sex="Mixed population"
/tissue_type="Entire tendril, 1
/dev_stage="At blooming"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Vitis shuttleworthii L., grape"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
XhOI; A high quality EST with at least 100 contiguous
bases at Trace Tuner score of 20 or better. Construction
by PM Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft.Pierce, FL, USA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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541.50
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RESULT 11
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Gardner MJ
The Institute for Genomic |
9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onygenales; mitosporic Onygenales; Coccidios 1 (bases 1 to 750)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO028609 750 bp mRNA linear 1
EST806993 Coccidioides posadasii spherule cDNA libra:
kb Coccidioides posadasii cDNA clone CIFAS82 3' end,
CO028609
CO028609.1 GI:48559837
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Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Bu
Eukaryota; Fungi; Onygenales; Coccidioides.
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      (1-686) x CO028609
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                            gardner@tigr.org.
Location/Qualifiers
                                                                                                                                                                                /note="Vector: pExpress 1; Site 1: Not I; Site Coccidioides posadasii spherule cDNA library, kb "
                                                                                                                                                                                                                                              /dev_stage="spherules"
/lab_host="E. coli DH10B,
/clone_lib="Coccidioides
                                                                                                                                                                                                                                                                                                                            /organism="Coccidioides
/mol_type="mRNA"
/strain="C735"
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/clone="CIFAS82"
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Cole.R., Fogarty,S., Tang,K., Howe,D.K., Sibley,L.D., Clifton,S. Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J., Ronko,I., Tsagareishvili,R., Fedele,M., Belaygorod,L., Franklin,C., Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Richey,J., Waterston
                                                                                                                                                                                         Neospora caninum
Eukaryota; Alveolata; Apicomplexa; Coccidia;
Sarcocystidae; Neospora.
Contact: Sandy Clifton, Ph.D. - USDA-WashU Neospora EST Project Washington University School of
                                               and Wilson,R.
USDA-WashU Neospora EST Project
Unpublished (2000)
                                                                                                                                                                                                                                           Neospora caninum
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Waterston,

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Percent Similarity:
Best Local Similarity:
Query Match:
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Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                              GlyAlaProLysLysArgThrMetGluIleIleAspArgLeuGluGluGlyProArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValArgAsnAspLeuAsnSerValCysAlaIleGlySerValHisValProArgLeuPhe
                                 IleArgThrIleVal
                                                                                                                                                                       ValTyrSerGlyAlaLeuGlyTrpPheAlaLeuSerGlyAlaAlaAspLeuSerIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ProGlyThrSerThrAlaAlaCysValArgAlaAlaPheProGlyGlySerMetThr
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                                                                                                           ATCTATAGCGGGGCGACTGGCTTCCTGTCGGTCACAGGTGAAGCCAGTTTAAACATCGTC
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//lab_host="ElectroTen Blue cells (Stratagene)"
//clone_lib="Nc-LIV Tachyzoite cDNA Library"
//clone_weivector: pBluescript II Sk-Vector type: plasmid;
//note="Wector: pBluescript II Sk-Vector type: plasmid;
//note="Wector: pBluescript II Sk-Vector type: plasmid;
//note="Wector: pBluescript II Sk-Vector type: plasmid;
//note="Wector: pBluescript II Sk-Vector type: plasmid;
//note="Wector: pBluescript II Sk-Vector, was synthesiszed from Poly(A)+ mRNA using
//note="Bluescript II Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Medical Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Medical Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Wector, and type: plasmid; was synthesis; EcoRI Blue cells (Stratagene).
//note="Wector type: plasmid; was synthesis; EcoRI iI Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Wector type: plasmid; was synthesis; EcoRI iI Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Wector type: plasmid; was synthesis; EcoRI iI Sk-Vector, and electroporated into ElectroTen Blue cells (Stratagene).
//note="Wector type: plasmid; was synthesis; electroTen Blue cells (Stratagene).
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//note="Wector type: plasmid;
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/mol_type="mRNA"
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AW509018
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  US-10-089-514-2 (1-686)
                                                                            Query Match:
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                                                                                                        Similarity:
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Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,J., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
MCCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: BE823672 corresponding to Gm-r1070-8099 (3') Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW509018 528 bp mRNA linear EST 24-JUL-2004 si39b01.y1 Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-r1030-1250 5' similar to TR:Q9ZV26 Q9ZV26 SIMILAR TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 337.
Location/Qualifiers
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Fax: 314 286 1810
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                  /note="Vector: pSPORT1; Bite 1: Sal1; Site 2: Not1; This cDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. Ball linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into be coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Gm-r1030 is a re-rack of Gm-c1007."
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/mol_type="mRNA"
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                                                                                                                                            Department of Eukaryotic Rockville, MD 20850, USA Tel: 301-838-3543
                                                                                                                                                                                                    End sequencing of clones
JEC21 cDNA library
Unpublished (2003)
Other_ESTs: CCAFB09TR
                                                                                                                                                                                                                                                                                 Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
                                                                                                           Seq
                                                                                                                       Fax: 301-838-0208
Email: crypt@tigr
                                                                                                                                                                                         Contact: Brendan Loftus
                                                                                                                                                                                                                                                    Loftus, B.
                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans var. neoformans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAGATCAATGGAACTTCTTGATTCTATTGAAAGTTGTTCTCGAGGTATCTACTCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGTACACGAGGGTGAAGCTTCAATAGGAGCTGGACGGGCAATGGTTGCTCTGTCAAAC
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                                                                                                          il: crypt@tigr.org
primer: TF.
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/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="JEC21"

/db_xref="JEC21"

/clone="CCAFB09"

/clone="CCAFB09"

/clone_lib="C.neoformans strain JEC21"

/note="Vector: pCMVSport6; Site_1: Not1_EcoRV; The
                                                                                     Location/Qualifiers
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length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

lignment S red. No.: core: ercent Sim est Local uery Match B:	Scores: 1.07e-36 Length: 890 1.07e-36 Matches: 117 1.01e-36 Conservative: 38 1.02e-36 Conservative: 38 1.02e-36 Conservative: 38 1.02e-36 Conservative: 42 2.5h: 13.99% Mismatches: 83 2.5h: 13.99% Indels: 42 2.5h: 7
S-10-089-5	\$14-2 (1-686) x CF703510 (1-890)
У д	146 ProThrGluAlaThrAlaLeuProLeuTyrSerAlaLeuArgAlaIleSerProValPro 465
У В 8	166 TyrGlyAlaLeuLeuGluPheProGluLeuSer
У 4	77
7	83
y 4 b 7	192 GlyGlyValGluSerLysProIleLysGlyfhrArgProArg
У 5	06 508
6	48
У 5	09AlaGluGluAspGluArgLeuArgÀlaAspLeuAlaGlyArgGluLysAspArg 526
	88 GAAGGGAGAAGGGATGAGCGAAGAGGGAGAGAATTGGTTGAAGATGTCAAAGAAG
	27 AlaGluAsnLeuMetIleValAspLeuValĀrgAsnAspLeuAsnSerValCysAlaIle 54
5	28 G
У 5	47 GlySerValHisValProArgLeuPheGluValGluThrTyrAlaP
4	68 TCAACAGTCACCGTTCCAAAACTTATCGCTCTTGAATCCTATGGGGTGCATAACC
Y 5	67 ValSerThr1leArgGlyArgLeuArgProGlyThrSerThrAlaAlaCysValArgAla 586
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	87 AlaPheProGlyGlySerMetThrGlyAlaProLyBLySArgThrMetGluIleIleAsp 6
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	91 GAGTTTGAGAACCATCAGCGAAGGGGCGTATACTCCGGTGCTTTGGGTTACTTTTCTGTC 23
Υ 6	26 SerGlyAlaAlaAspLeuSerIleValIleArgThrIleValLeuAlaAspGlyGlnAla 645
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٧	46 GluPheGlyValGlyGlyAlaIleValSerLeuSerAspGlnGluGluGluPheThrC
Б	71 AGTATCGGGGCTGGAGGTGCCATCACCTGGCTATCGGATAGGGAGAAGGAATGGGATGAG 112
,	ValLysAlaArgAlaMetValThrAlaLeuAs
6	11 GTGTTGACCAAGGTGAAGTCTGTAGTTGGAAGAATAGAGGATGGAGAATGACATGCTG
ESULT 15	

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Rockville, MD 20850, USA Tel: 301-838-3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptococcus neoformans var. neoformans Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Filobasidiella.
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CF704316.1 GI:41558475
EST.
Cryptococcus neoformans var.
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Other_ESTs: CCACN30TR
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JEC21 cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: crypt@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loftus, B.
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                                                                                                                                   CAATGTATATGTCGACCTGGCATCGGGTGTGGGGGAGAAAACCCCAGGCTCGGTGGAGTGC
                                                                                                                                                                               TCAGGAACACAGGGTATCACCATCCTCTCAAGTTCTCCTGAACGGTTCTTGAAAATCAAC
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AAACAGGAAGGGAGAAGGGATGAGCGAAGAGGGAGAATTGGTTGAAGATGTCAAA
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/clone=lib="C.neoformans strain JEC21"
/clone=lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full length, normalized library was prepared from a variety conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Cryptococcus"
ool_type="mRNA"
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                                                          GATGAGGTGTTGACCAAGGTGAAGTCTGTAGTTGGAAGAATAGAGGATGGAGAATGACAT
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Search completed: October 5, 2005, 18:37:41
Job time: 7524.63 secs

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Result
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 1
BD178314
LOCUS
DEFINITION VERSION KEYWORDS ORIGIN FEATURES COMMENT ACCESSION AUTHORS
TITLE
The same and novel biosynthetic gene
Patent: WO 02077244-A 2 03-OCT-2002;
PM WO 02077244-A/2
PD 03-OCT-2002
PF 22-MAR-2001 TF
PR 22-MAR-2001 TF
PR 22-MAR-2001 TF
PR 22-MAR-2001 TF
PR 22-MAR-2001 TF JOURNAL source Transformant producing PF1022 substance and the same and novel biosynthetic gene.
BD178314
BD178314 GI:30015579
WO 02077244-A/2. SHE 1222 and Key CDS MURAKAMI C12N15/61,C12N1/15,C12P17/14//(C12N1/15,C12R1:645),(C12P17/14,C12R1:645) Transformant producing PF1022 substance and process for 22-MAR-2002 WO 2002JP002782 22-MAR-2001 JP 01P 082227 KOJI YANAI,NAOMI SUMIDA,MANÁBU WATANABE,TATSUKI MORIYA,TAKESHI producing the same novel biosynthetic gene Location/Qualifiers (1)..(309). /organism="Streptomyces
/mol_type="genomic DNA"
/db_xref="taxon:54571" Location/Qualifiers venezuelae" linear and Murakami, T. process for producing process PAT 16-APR-2003 for producing

a

Streptomy

Query Match

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nes 312; Conserv
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L Patent: WO 0123542-A, 2 05-APR-2001;
MEIJI SEIKA KAISHA LTD, KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA,
MANABU WATANABE, KOICHI MIYAMOTO, NAOKI MIDO, TAKESHI MURAKAMI

OS Streptomyces venezuelae
PN WO 0123542-A/2
PD 05-APR-2001
PF 29-SEP-2000 WO 2000JP006783
PR 29-SEP-2000 WO 2000JP006783
PR 29-SEP-1999 JP 99P 276314
PI KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA, MANABU WATANABE, KOICHI
PI NAOKI MIDO, TAKESHI MURAKAMI
PC C12N15/09, C12N5/10, C12P21/02, C07K11/00// (C12P21/02, C12R1:645)
FT CDS Location/Qualifiers

FT CDS Location/Qualifiers
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WO 0123542-A/2.
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ilarity 100.0%;
Conservative 0
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/mol_type="genomic DNA"
/db_xref="taxon:54571"
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                                                                                                                                                                                                                                                                                                                                                       Submitted (01-AUG-2003) Koji Yanai, Meiji Seika Kaisha, Microbiological Resources and Technology Laboratories; Odawara-shi, Kanagawa 2500852, Japan (E-mail:koji yanai@meiji.co.jp, Tel:81-465-37-5106, Fax:81-465-37-6397)
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nai, K., Sumida, N.,
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CGGCACGGCGTCCCCGATGATGCAGCCCGGCCCGCGTCAGCCTGGTCAAGGACAGGGCCGCC
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                                                                                                              CTCCTGGACACGGTGCGGCGCGCATCGACCTCGGTGTCCGCATCGCGCGGTACAAGTCC
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St, Halifax, NS B3H 4JI, Canada
Sequence update by submitter
On Jun 5, 2001 this sequence version replaced
Location/Qualifiers
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The gene cluster for chloramphenicol biosynthesis in Streptomyc venezuelae ISP5230 includes novel shikimate pathway homologues a monomodular non-ribosomal peptide synthetase gene Microbiology 147 (Pt 10), 2817-2829 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-MAY-2000) Biology, St, Halifax, NS B3H 4J1, Canada 3 (bases 1 to 14159)
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He,J., Magarvey,N.A. and Vining,L.C
Direct Submission
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces venezuelae chloramphenicol biosynthetic gene cluster, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                  map="adjacent to pabAB"
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                                                                                                                                                                                                                                                                                                                                                                                              function="essential for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Streptomyces
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                                                                               GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGCCTGACGGC
                                                                                                         GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGCCTGACGGC
                                                                                                                                                                                             CGCCCGCTACGCCGCCGACCACGGCCTCGACGAATCGTTCCTGGTGAACCTCTACGACGT
                                                                                                                                                                                                                                                      GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
                                                                                                                                                                                                                                                                                              GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
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CGAGGACCGGCGGTGA 11457
                                     CGAGGACCGGCGGTGA
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/note="Region: 6

4350. .4370

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4494. .4538
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3708. .3746
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3576. .3596
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4893. .4910
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4833. .4853
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4647. .4706
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4593. .4610
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98.4%;
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Sequence
A48325
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Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F., Crouzet, J.,
Barriere, J.-C., Debussche, L., Famechon, A., Paris, J.-M. and
Dutruc-Rosset, G.
                                                     Streptogramins for preparing Patent: US 6352839-A 4 05-MAI
                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                         Sequence 4 from AR198355
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Barriere, J., Debussche, L.,
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                Unclassified.
                                                                                                                                                                                                      Unknown
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publication FR 2722210 960112
Location/Qualifiers
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                    Location/Qualifiers
1. .387
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/mol_type="unassigned DNA"
/db_xref="taxon:38300"
organism="unknown"
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from Patent WO9601901
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Pred. No. 2.5e
0; Mismatches
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Matches 183;
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Sequence 1 from Patent WO9601901.
A48323
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1 (bases 1 to 2888)
Blanc, V., Thibaut, D., Bamas Jacques, N., Blanche,
                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces pristinaespiralis
Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                         Dutruc-Rosset,G.
STREPTOGRAMINES AND METHOD FOR PREPARING
                                                                                                                                                                                                                                                                                                                                                               Barriere, J., Debussche, L.,
                                                                                                                                                                                                                                                                                                                   Patent: WO 9601901-A 1 25-JAN-1996; RHONE POULENC RORER SA (FR)
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                                                                                                                               ACCCCTCGACGCGCGCGCGCCCGGCCGGACGCCGGCCCTGCTGGACGCCG
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                                     CGATGATGCAGCCCCACCGGATCGCCCAGGTCCACGCCAACGCCGCCGCCTACGCCGCCG
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                                                                                                                                                                                                                                                                                          publication AU 2891295 960209 publication FR 2722210 960112
                                                                                                                                                                                                                                   /organism="Streptomyces pristinaespiralis"
/mol_type="unassigned DNA"
/db_xref="taxon:38300"
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69.8%;
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Pred. No. 2.5e-09;
0; Mismatches 79;
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Pred. No. 1.5
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Blanc, V., Thibaut, D.,
                                                1 (bases 1 to 4740)
Blanc, V., Gil, P., Ba
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                         Thibaut, D.
                                  Schleuniger,J.,
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Streptomyces pristinaespiralis
Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Streptomyces pristinaespiralis 4-dir
precursor biosynthesis (papA, papC,
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Identification and analysis of genes from Streptomyces pristinaespiralis encoding enzymes involved in the bio
                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae;
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/mol_type="unassigned
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patent US 635
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Pred. No. 1.5
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Blanche,F., Debussche,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-dimethylamino-L-phenylalanine papC, papB, papM) genes, complet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                             /translation="WRGGSVFGRCVVVGGAGAVGRMFSHWLVRSGVAVTWLDVAGAGA
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LARIAGGTPEVYFDIQAANPGAPAARQALGRGLVRLGQAVERGDEETFAALFAELRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAPAAERWLTDAARTLATTAPRPPFTILLPDDQLPALDVHYRHSLPRYRELVEECRRL
ITDGETYEVCLTNMLRVPGRIDPLTAYRALRTYSPAPYAAYLQPPGATYLSSSPERFL
RIGADGWAESKPIKGTRPRGAGPAQDAAVKASLAAAEKDRSENLMIVDLVRNDLGQVC
DIGSVHVPGLEEVETYATVHQLVSTVBGRLAADVSRPBAVRAAPPGGSMTGAPKVRTM
QFIDRLEKGPRGVYSGALGYFALSGAADLSIVIRTIVATEEAATIGVGGAVVALSDPD
DEVREMLLKAQTTLAALRQAHAGATASDRELLAGSLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHRHLERFGVQFHESISSEHGHRMLANFRDLSLRAAGHRPHTERIPAPAPAPAPA
APAPRASAPVGEYLHVREVACVPDADAAFTJALFADAPAFRIDSSRVEBGLARFTFL
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GAPAGFLGEOITYDVADATAVBVKOGSGGETRRFGTLFPHLEHELAARALPATGLIPEF
NLGYVGYLGVETKADSGGEDAHRGELPDGAFMFADRMLALDHEQGRAWLLALSSTRRP
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                                                                                                       /translation="mtppa1paappatgpaaatdpldalrarldaadaalldavrtrl
DICLRIGEYKRLHQVPMMQPHRIAQVHANAARYAADHGIDPAFLRTLYDTIITETCRL
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68. .2227
                                     /gene="papM"
3799. .4677
                                                                                                                                                                               /codon_start=1
/transl_table=11
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3413. .3802
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/db_xref="GI:1575337"
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/function="p-aminobenzoate
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/gene="papM"
/function="N-methylase"
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/function="mutase"
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/transl_table=11
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/db_xref="GI:1575336"
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db_xref="GI:1575338"
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mol_type="genomic DNA"
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Streptomyces griseus subsp. griseus
Streptomyces grieeus subsp. griseus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                            Submitted (02-MAY-2000) Chemistry, Davis, One Shields Ave., Davis, CA Location/Qualifiers
                                                                                                                                                                                                                                                                     2 (bases 1 to 10029)
Smith, W.C., Xiang, L. and Shen, B.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 10029)
Smith, W.C., Xiang, L. and Shen, B.
Genetic localization and molecular characterization of the nonS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces griseus subsp. griseus macrotetrolide biosynthesis gene cluster, downstream region.
                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                       griseus DSM40695
                                                                                                                                                                                                                                                                                                                                                                                                          gene required for macrotetrolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 1.3e-09;
0; Mismatches 79
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                                                                                                                                                                                                   University
95616, USA
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LAVQAHGWELGLRSGYLPPELLGTPDALRRAGESRTNNLGGWYAK"
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TREGLRRPGDIGISTYLFFRTVADALPDEAGDAVVAAVRRTLLAEGRAVLGRAQAED
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DRDTASRPAEERR"
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IEALADSLGAAVGASRAAVDAGWYPHTSQVGQTGKSVSPQLYIASGISGAIQHRAGMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (5438. .6403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APGAEDTDAPAAERLSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="amino acid decarboxylase-like protein"
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/codon_start=1
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/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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뭐 S 밁 δ 문 S 밁 S 뭉 Ş 밁 S

DasSarma,S

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                             DEFINITION
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Ng, W.V., Kennedy, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Swartzell, S., Weir, D., Hall, J., Dahl, T.A., Welti, R., Goo, Y.A., Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocke, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ebhardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and
                                                                                                                                                             Halobacterium sp. NRC-1
Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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AE005068 AE004437
AE005068.1 GI:10581033
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                   Dennis, P.P.,
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Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weitr,D., Hall,J., Dahl,T.A., Weltri,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.B., Krebs,M.P. Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.,
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-JUL-2000) Institute for Systems Roosevelt Way NE, Seattle, WA 98105, USA
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Proc. Natl. Acad. Sci. U.S.A. 97 (22), 12176-12181 (2000)
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                                                                                                                                                                                              complement (1776. .2588)
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complement (1776. .2588)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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3984. .4850

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7658. .7906
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Horti, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Horti, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Mikara, J., Miyazaki, A., Mizuno, K., Murakami, K., Nurata, M., Nagata, T., Nakahama, Y., Nakamura, M., Numasaki, R., Ohno, M., Ohisuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shibata, X., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Tagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sano, H., Sakai, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Yohomizo, S. and Yoshimura, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yohomizo, S. and Yoshimura, A.
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Tsunoda, Y., Ueda, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Cent and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
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Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
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Tel:81-29-838-7007, Fax:81-29-838-7007
Tel:81-29-838-7007, Fax:81-29-838-7007
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                                                                     Matsubara, K. and Murakami, K. n Riken Genomic Sciences Center
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PUBMED
REFERENCE
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SOURCE
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                                                                     JOURNAL
MEDLINE
                                                                                                                                          TITLE
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                                                                                                                                                                                       Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium sp. NRC-1
Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kishikawa-Hirozane, T., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, M., Nishi, K., Numasaki, R., Ohno, M., Osato, Notara, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., Nishi, M., 
                                                                                          Genome sequence of Halobacterium species NRC-1
Proc. Natl. Acad. Sci. U.S.A. 97 (22), 12176-12181 (2000)
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AE005050 AE004
                                                                                                                                                                      DasSarma
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      (bases 1 to 16905)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16905 bp DNA linear BCT 12-FEB-20 erium sp. NRC-1 section 81 of 170 of the complete genome.
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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•
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SGD
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Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.,
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUL-2000) Institute for Systems Biology, 4225 Roosevelt Way NE, Seattle, WA 98105, USA
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                                                                                                                         /product="stationary phase survival protein"
/protein_id="AAG19603.1"
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Best Local S
Matches 120
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                         AP006840 08
AP006840 10
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AP006840 12
AP006840 13
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Appon6840 01
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Appon6840 04
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RIEAAFGTNETADNTTTLDNSSAASVARP"
Complement (8313. .11153)
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VDEVHELAGAKRGAQLAIGLERLVEVAGRVQRIGLSATVGDPHEIGAFLTGGRGCEII
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3. .11153)
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Streptomyces coelicolor A3(2) complete genome; segment 17/29.
AL939120 AL078618 AL160312 AL160431 AL353815 AL356334 AL392146
AL392148 AL392175 AL392176 AL392178 AL645882
                  2 (bases 1 to 248550)
Bentley, S.D.
                                                                                                    Complete genome sequence of the model coelicolor A3(2)
Nature 417 (6885), 141-147 (2002)
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On or before Oct 26, 2002 this sequence version replaced gi:11595527, gi:7242710, gi:7248323, gi:20520808, gi:7981386, gi:10129696, gi:10129727, gi:10178320, gi:10178340, gi:10178373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SC6F11.11c, probable araC family transcriptional regulatory protein, len: 344 aa; highly similar to TR:Q9S166 (EMBL:AB023785) Streptomyces griseus AdpA, 405 aa; fasta scores: opt: 881 z-score: 1024.1 E(): 0; 46.9% identity in 322 aa overlap and to TR:CAB70646 (EMBL:AL137242) Streptomyces coelicolor putative transcriptional regulator SC6F4.20c, 337 aa; fasta scores: opt: 1237 z-score: 1238.7 E(): 0; 60.3% identity in 325 aa overlap. Contains Pfam match to entry PF00165 HTH AraC, Bacterial regulatory helix-turn-helix motif at residues (family and a possible helix-turn-helix motif at residues 249. .270 (+2.55 SD)"
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/gene="SCO4413"
/note="syronym: SC6F11.1
complement(1200..2234)
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protein"
                2305. .2308
2319. .3644
                                                   /note="Pfam match to entry PF00165 HTH_AraC, Bacte)
regulatory helix-turn-helix proteins, araC family,
74.90, E-value 1.6e-18"
                                                                                                                         complement (1233.
/gene="SCO4413"
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/protein_id="CAC08421.1"
/db_xref="GI:10178383"
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identity in 135 aa
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/mol type="genomic DNA"
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/translation="MADSTASAEPQRPTHPAGRPVYVIGAGPGGLAVAHALRARGLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SC6F11.14c, probable monooxygenase, len: 401 aa; similar to TR:Q95DE6 (EMBL:AP000837) Oryza sativa similar to human dimethylanilyne monooxygenase, 437 aa; fasta scores: opt: 692 z-score: 722.8 E(): 9.3e-33; 38.2% identity in 403 aa overlap. Contains Pfam match to entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="UniProt/TremBL:Q9F373"
/translation="MGMGTEPSAAEGRELPWSNDEWNVAAALCATQLPLMWLAWWFFV/translation="MGMGTEPSAAEGRELPWSNDEWNVAAALCATQLPLMWLAWWFFVGAGGLDHLFULPLLPRRSGPEWARHVVAGAGGDDHGRGGAGFGVLCLPLVFLDLGVVHSSAQIMPAATLARLLPRRSGEWKVWLRSAGAGLVCAGWAVLGHLVWGWPPRDTVPWFAGAGILPVLFLAPLRRAWGGWSVWLRSAGACTUVCAGWAVLRLAPGGRAGLTRVPSRACFULSVAGGLAVAALADEYEPPALSDGQLAGEWRGDHGAVLRLAPGGRAGLTRVPSR
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                                                                                         complement (4754.
                                                                                                                                               VVLERADHVGSSWRRHYDRLRLHTTRRLSALPGLPIPRRFGRWVARDDVVRYLEKYAE YHQLEIVTGVBVFRVERAPDGTGWLHAAGGRELTGAAVVVARGYNHTPRVPDWPGRD TYTGEFRHAADYRTPAPPAGRDVLVVGVGNTGAEIAVDLYGGAARVRLAVTAPHIV TRTGEFRHAADYRTPAPPAGRDVLVVGVGNTGAEIAVDLSAQGLPRFCTGLYSRVAEG RRSTRAWAAQYTGVLCRRLFVALUDRLARPLARISVPDLSAQGLPRFCTGLYSRVAEG AIPVQDVGLIDAVRSGRVEVVAAMDGFEDGKVLLADGTRIAPDAVIAATGYRRGLEGL VGHLGVLDGTGRPVVQGGRTPAAAPGLYFTGFTNPISGMLRELAIDAERIAGAVAKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity in 403 aa overlap. Conta
pF00743 FMO-like, Flavin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: SC6F11.14c"
complement(4721..5926)
/gene="SC04416"
/note="SC6F11.14c, probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4721. .5926)
/gene="SCO4416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDFGTYRDYTRCSGTGTWSRNLSGDREGVVVRLDGDCGEETSWTIGGSERSPELFALF
GDPDAGDLLFLTRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCO4415"
/note="SC6F11.13,
290 aa. Contains I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: 3666. .4538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3666
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TGVLTAASASGQLIFLELLSWIVETYDWFAAVTVALAALAVVETVMLLLHDHBADVG
QKPYGAKEFVPKPAFVFAARRALTVLFAAVETGEFWILAGTEAIGAGSTTGLIGTHS
VBAAHDHGMFITAAASLLAVIGVFDVAGTIASGWFTDRFEPRRLLAVYYALRGVSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTQTTDAAAAAASEARPEPTRPGRPTRAHRAWWVAAVTFVTII
GAAAFRSLPGILIDPLHQEFGWSRGTIGAAVSVNLALYGLTAPFAAALMDRFGIRRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SC6F11.12, possible integral membrane protein, len 441 aa; similar to TR:BAB06413 (EMBL:AP001516) Bacillus halodurans transporter BH2694, 418 aa; fasta scores: opt: 795 z-score: 909.8 E(): 0; 31.0% identity in 413 aa
Flavin-binding monooxygenase-like,
                                                                                                                            AGGVSRLPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions"
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2319. .3644
                                                               /gene="SCO4416"
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/note="SC6F11.12,
                               'note="Pfam match to entry PF00743 FMO-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="SC04415"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC6F11.13"
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423.1"
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   score -255.00,
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Best Local
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                                                                                                                                                              185444 CGGCTACTTCATCAACCCGCTGGTCACCATCGCGATGGGCGTG
                                                                                                                                                                                                                                                                                                                                 185504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185624 GTGGTCCCTCGCCTTCGTCGCCGTCGCCCTCCTTCGTACGGCGCTGGGCCTGGGCCGG
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                                                                                                                                                                                                                                              GATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGCCTG
                                                                                                                                                                                                                                                                                                                             CGTCAACTGGGGCGTCTACATCTGGGCCGTGAACAGCGGCCATGTCGTCGAGGCCTCGCT 185445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGCTGCTGCGCAGCCGCGCAGGCTCGCCCTGGTCGCGGTGGCCGCCGCCGCTCATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/translation="WAHTPMYTLDF"/
/translation="WAHTPMYTLDF"/
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/translation="WAHTPM
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ERSGYVVEGTLREAMFEAGRHDAPRDVHLHARLATDEEPTPPGAR"
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/gene="SCO4417"
/note="synonym: SC6F11.15"
6026. .6643
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Pred. No. 3
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                                                                                  Score
                            53.6
53.6
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1: geneseqn1980s:*
2: geneseqn1990s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Claim 13; Page 65; 83pp; Japanese

Transformant producing secondary metabolite modified with functional group e.g. benzene with nitrogen-containing substituent at para-position, PF1022, with ease at low cost, for application in pharmaceuticals and agrochemicals.

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22-MAR-2002; 2002WO-JP002782
                                                        03-OCT-2002
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                                        DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; Tyrk: orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel biosynthesis gene-transferred transformants for producing PF1022 substance derivatives by fermentation, as pharmaceuticals or veterinary drugs with anthelmintic activity.
                                                                                                 Plasmid papABC
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                                                                                                                                                            ABZ69799;
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                                                                                                                                                                                                                                                              GACCGGCGGTGA 312
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                                                                                                                                                                                                                                                                                                                       ATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGCCTGACGGCCGAG
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                                                                                                                               (first
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                           p-aminophenylalanine;
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                                                                                                                                                                                      DNA;
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Pred. No. 1.4e-46;
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                           pAF; chorismate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>.
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Synthetic biosynthesis;

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Aspl2TAG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is provided exogenously. The translation system is a cell and the unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid containing the individual genes papABC that encode the enzymes used to carry out the conversion of chorismate to the unnatural amino acid p-aminophenylalanine (pAF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-tRNA with at least one unnatural amino acid in the translation system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and the O-tRNA recognises at least one selector codon. A composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4;
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06-FEB-2002;
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                                                                                                                                                          GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGAGCCTGACGGC
                                                                                                                                                                                                                                                              GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
                                                                                                                                                                                                                                                                                   GTCCCGGCACGGCTCCCGATGATGCACCCCGGGCCGGGTCAGCCTGGTCAAGGACAGGGC 176
                                                                                                                                                                                                                                                                                                                             GACGCTTCTGGACACGGTGCGGCGCGCATCGACCTCGGTGTCCGCATCGCGCGGTACAA
                                                                                                                                                                                                                                                                                                                                                                                                              ATGACCGAGCAGAACGAGCTGCA----GCGGCTGCGCGCGGAGCTCGACGCCCTCGACGG 56
                                                                                                                                        GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGGAGAGCCTGACGGC 3285
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                                                                                                         CGAGGACCGGCGGTGA
                                                                                                                                                                                                  CGCCCGCTACGCCGACCACGGCCTCGACGAATCGTTCCTGGTGAACCTCTACGACGT
                                                                            CGAGGACCGGCGGTGA 3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 127-128; 188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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, Pastrnak M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%;
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                                                                                                         1 312
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Pred. No. 6.6e-44;
0; Mismatches 1;
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y orthogonal tRNA and orthogonal
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ABZ69798 standard; DNA; 12391 BP

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Matches 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schultz
Meggers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; TyrRS;
orthogonal aminoacyl tRNA synthetase; unnatural amino acid;
chloramphenicol acetyltransferase; dihydrofolate reductase; ds; plasmid;
                                                                                                                                                                                                                                                              Sequence 12391 BP; 2830 A; 3588 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aminoacyl tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful for producing protein comprising unnatural amino has translation system comprising orthogonal tRNA and orthogonal
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06-FEB-2002; 2002US-0355514P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 124-127; 188pp; English:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biosynthesis; p-aminophenylalanine; pAF.
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                                                    GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
                                                                                             GACGCTCCTGGACACGGTGCGGCGCGCCATCGACCTCGGTGTCCGCATCGCGCGGTACAA
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                                     GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
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, Mehl RA,
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97.9%;
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                                                                                                                                                                                                                                                                             The papA and papM genes of S.pristinaespiralis are involved in the biosynthesis of 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor for pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papC) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The PapC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DMPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is cleavy 4-aminoprephenate acid. Disruption of the papB and papC genes can be used to produce strains of S.pristinaespiralis which are unable to produce the antibiotic pristinamycin I but which may be able to produce con the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produce of the produ
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Matches 183
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P-PSDB; AAW11583.
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                                                                                                                                                                                                                          Sequence
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                                                                                                   al Similarity
183; Conserv
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                                                                                                   Conservative
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L, Famechon
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Pred. No. 2.3e
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Paris J,
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Dutruc-Rosset
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New streptogramin B derivs. useful as antibiotics - produced by mutants of Streptomyces having altered genes for streptogramin E
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          biosynthesis.
                                                                                         Blanc V,
                                                                                                                                                    04-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces pristinaespiralis.
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                                                  P-PSDB;
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                                               1996-097631/10.
DB: AAW11582, AAW11583.
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                                                                                         Thibaut D,
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1. .687
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/note= "C-terminal
                                                                                                                                                                                                                                 product= "PapM"
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|873. .2262
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e L, Famechon A,
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Best Local Similarity
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                                                                                                  28-MAR-2001; 2001US-0279095P.
30-MAR-2001; 2001US-0279709P.
20-APR-2001; 2001US-0285214P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthosomycin biosynthetic polynucleotide SEQ
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  Farnet
                                                                                                                                                                                                            28-MAR-2002; 2002WO-CA000432
                                                                                                                                                                                                                                                                10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                     Streptomyces mobaraensis
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                                                   (ECOP-) ECOPIA BIOSCIENCES INC
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Zazopoulos E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; everninomicin; avilamycin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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69.8%;
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  Staffa
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Pred. No. 1.9e
O; Mismatches
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1.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ666813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABP99207-ABP99362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene cluster. The method is useful for detecting the presence of any organism that contains DNA for the production of orthosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new
28-MAR-2001; 2001US-0279095P.
30-MAR-2001; 2001US-0279709P.
                                              28-MAR-2002;
                                                                                                                                          Streptomyces mobaraensis
                                                                                                                                                                          Orthosomycin; biosynthesis;
                                                                                                                                                                                                       Orthosomycin biosynthetic gene cluster SEQ
                                                                                                                                                                                                                                                                                                     ABZ66808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying orthosomycin biosynthetic gene, gene fragment cluster, by detecting presence of nucleic acid sequence of 17 of flambamycins protein families.
                                                                                                            WO200279505-A2
                                                                                                                                                                                                                                        21-MAR-2003
                                                                                                                                                                                                                                                                        ABZ66808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1458 BP; 229 A; 530 C; 491 G; 208 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orthosomycin natural products,
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P-PSDB; ABP99244.
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                                                                                                                                                                                                                                                                                                    standard; DNA; 45055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGCTGGTCCAGGAGAACCCGACCGTCCGCGACCTCATGGCGGAGGGCGAGTACCAGCC 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCGTCCGGGTGGAGCAGGACTTCTCCTACGTCGCCGACAGCTTCCACGGCCCCGGCTA
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                                               2002WO-CA000432
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%;
                                                                                                                                                                          everninomicin; avilamycin;
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0; Mismatches
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Pred. No. 0.
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                                                                                                                                                                                                         NO 277.
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                                                                                                                                                                          gene;
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RESULT 9
ABD12889
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Best Local Sim
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ66813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABP9207-ABP9362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene fragment or gene fragment or gene fragment or gene fragment or gene cluster. The method is useful for detecting the presence of any organism that contains DNA for the production of orthosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new
                                   US6551795-B1
                                                                                                                                         Pseudomonas aeruginosa polynucleotide #11493.
                                                                                                                                                                                                                                      ABD12889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45055 BP; 6228 A; 16576 C; 16043 G; 6208 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying orthosomycin biosynthetic gene, cluster, by detecting presence of nucleic ac
                                                                Pseudomonas aeruginosa
                                                                                              antibacterial
                                                                                                              Bacterial
                                                                                                                                                                         29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orthosomycin natural products, not produced by the organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uster, by detecting presence or in
of flambamycins protein families.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                GGCGCTCTACAGCGGCATGCTGGCCGCGACGTCCGTGCTCGCCACGGTGAACGAGGAC 37332
                                                                                                                                                                                                                                                                                                                                                                             CTACCTCGCCGGCGACGCCTGCTTCCTCGACCCGCTGCTGTCCACCGGCGTCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCGCTGGTCCAGGAGAACCCGACCGTCCGCGACCTCATGGCGGAGGGCGAGTACCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACACGGTGCGGCGCGCATCGACCTCGGTGTCCGCATCGCGCGGTACAAGTCCCGGCA
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                                                                                                                                                                                                                                                                                                                                             GGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCGGGAGAGCCTGACGGCCGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                         CGCCGCCGACCACGGCCTCGACGAATCGTTCCTGGTGAACCTCTACGACGTGATCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCGTCCCGATGATGCAGCCCGGCCGGCTCAGCCTGGTCAAGGACAGGGCCGCCGCTA
                                                                                                           infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 425-450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zazopoulos
                                                                                                                                                                        (first entry)
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54.8;
Pred. No. 0.
                                                                                                           Pseudomonas aeruginosa infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e, gene fragment or gene acid sequence correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152;
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RESULT 10
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ID ABD128
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AC ABD128
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                Pseudomonas aeruginosa polynucleotide #11423
                                                29-JUL-2004
                                                                                                           ABD12819 standard;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequence of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polypucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 11493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html
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389
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CGATGGCAGCCTGGCCGCGACCCTCAAGGACGGCCGG
                                      GATGAGCCGGGAGAGCCTGACGGCCGAGGACCGGCGG
                                                                                                                      GTTCCTGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCGAGGACCTGGT
                                                                                                                                                               TCGCGACCTGTTCCTGCGCGGCTTCGACCGCAGCGTCCGCGAGCATCTGCGCGACGAATT
                                                                                                                                                                                                        CGGTGTCCGCATCGCGCGGTACAAGTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCG
                                                                                                                                                                                                                                                                                                                                   CGAAGCGTTCTTCCTCGAGCGCCTGCCGCGCCGCATGCTTGGTCGGCGGCGGCGGCTACAT
                                                                               GGGCAAGAAGGGCCTGGACCTGCAGTTCAACAGCGACATCGCCCGTATCGACAAACAGGC
                                                                                                                                                                                                                                                 CGCCGTCGAGTTCGCCTCGATCTTCAACGGGCTCGGCGCCGAGACCACCTTGCTCTACCG
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49.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.6; DB Pred. No. 0.49;
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425
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(first entry)

DNA; 1359

ВP

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therefore therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as targets for actibacterial drugs, production of P. aeruginosa-derived peptides for recombinant components for diagnosis and/or treatment of P. aeruginosa-derived peptides, as target for polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD1397-ABD17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                               138;
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                                                                                                                                                                                     TCGCGACCTGTTCCTGCGCGCGCTTCGACCGCAGCGTCCGCGAGCATCTGCGCGACGAATT
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                                                                                         GATGAGCCGGGAGAGCCTGACGGCCGAGGACCGGCGG
                                                                                                                        GGGCAAGAAGGGCCTGGACCTGCAGTTCAACAGCGACATCGCCCGTATCGACAAACAGGC
                                                                                                                                                      GTTCCTGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCGAGGACCTGGT 272
                                                                                                                                                                                                                  GETCAGCCTGGTCAAGGACAGGGCCGCCCGCTACGCCGCCGACCACGGCCTCGACGAATC
                                                                                                                                                                                                                                                                                CGGTGTCCGCATCGCGCGGTACAAGTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCG
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98US-0094190P.
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Pred. No. 0.45
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0.45;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis a therapy of pathological conditions, as molecular targets for diagnosis prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant
                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                  1371 BP;
    GTTCCTGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCGAGGACCTGGT
                                                            GGTCAGCCTGGTCAAGGACAGGGCCGCCGCCTACGCCGCCGACCACGGCCTCGACGAATC
                                                                                          CGCCGTCGAGTTCGCCTCGATCTTCAACGGGCTCGGCGCCGAGACCACCTTGCTCTACCG
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                                  TCGCGACCTGTTCCTGCGCGGCTTCGACCGCAGCGTCCGCGAGCATCTGCGCGACGAATT
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98US-0094190P
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                                                                                                                                                                                                                       Score 54.6; DB Pred. No. 0.45;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                    DB 11;
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GGGCAAGAAGGGCCTGGACCTGCAGTTCAACAGCGACATCGCCCGTATCGACAAACAGGC

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	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	Key CDS	Actinoplanes t	ss; gene; tcp antibiotic; ba 5-dihydroxy-ph aromatic resid resistance; ch	tcp gene cluster	ADS73531;	RESULT 12 ADS73531 ID ADS73531 standard; XX	273 GATG <i>P</i> 726 CGATG
/"tag= 1 /label= ORF9 /note= "Required for synthesis of the heptapeptide skeleton"	<pre>/*tag= n /label= ORF8 /note= "Required for the addition and formation of N-acyl -beta-glucosamine residues" 1059716827 /*ter.</pre>	- u = "	S 5 5 5 7 - "	£ 5 - "	/ Label= ORF4 /label= ORF4 /note= "Required for export of teicoplanin outside of the /note= "Required for coferring resistance to teicoplanin" complement (56346173) /*tag= e	/ Label = Okr 3 /note= "Required for export of teicoplanin outside of the cytoplasm, and for coferring resistance to teicoplanin" 4264. 4872	/label= ORF2 /label= ORF2 /note= "Required for export of teicoplanin outside of the cytoplasm, and for coferring resistance to teicoplanin" 32274264 /*tag= C			Actinoplanes teichomyceticus; ATCC31121.	ss; gene; tcp; gene cluster; biosynthesis; glycopeptide; telcoplanin; antibiotic; bal; cep; com; sta; 4-hydroxy-phenylglycine; 3; 5-dihydroxy-phenylglycine; heptapeptide skeleton; cross-linking; aromatic residue; N-acyl-beta-D-glucosamine; core structure; export; resistance; chlorination; alpha-hydroxylation; mannosyl attachment.	er.	(first entry)	ard; cDNA; 73882 BP.	GATGAGCCGGGAGACCTGACGGCCGAGGACCGGCGG 309
FT CDS	ETT CDS	PT CDS	FT CDS	PT CDS	FT CDS	FT CDS	FT CDS	FFT CDS	FT CDS	FT CDS		FT CDS	FT CDS	FT FT CDS	CDS
/label= ORF24 /note= "Required for the addition and formation -beta-glucosamine residues" 5294854540	. "	• ₪ P- =	<pre>CORF21 "Required for the chlorination solution colorination color</pre>	• D) H- =	/note= "kequired for cross-linking of aromatic atposition 2 and 4, 4 and 6, 1 and 3, and 5 and telcoplanin" 4603847234 /*tag= t /*tag= t	1.46048 8 S S ORF19	/ label= ORF1/ 43696. 44871 /*tag= r /label= ORF18 /note= "Required for cross-linking of aromatic /note atposition 2 and 4, 4 and 6, 1 and 3, and 5 and	/label= ORF16 /note= "Required for export of teicoplanin cytoplasm, and for coferring resistance to 4337343585 /*tag= q	/IADEL= UKFI5 /note= "Required for attachment of mannosyl 4134343289 /*tag= p		/*tag= m /label= ORF13 3840139222 /*tag= n /label= ORF14	от вуниневтв	7873 RF12 Compared for complete of the	2005332256 /*tag= k /label= ORF11 /note= "Required for synthesis of the heptapeptide skeleton"	0 11

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/label= ORF27
58746. .59735
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/note= "Required for synthesis phenylglycine residues"
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71318. .72412
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/label= ORF25
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9083. .70180
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                                                                        The snaC gene product is involved in the biosynthesis of streptogramins, antibiotics active against Gram-positive bacteria. The identification of the sequences encoding the enzymes involved in the biosynthetic pathway means that they can be isolated and manipulated. Mutant microorganisms in which a step in the streptogramin biosynthetic pathway is blocked can be cultured to produce streptogramin intermediates, which may later be
                                                                                                                                                                                      DNA involved in streptogramin antibiotic biosynthesis - for -conversion of streptogramin(s) or prodn. of streptogramin i derivs. or hybrid antibiotics.
                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                 Claim 2; Page 54-55;
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                                                                                                                                                                                                                                                                                             Blanche F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
pathway; Streptomyces pristinaespiralis; ds.
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converted to streptogramin derivatives. Recombinant cells may also be used for the bioconversion of streptogramins from one form to another for the production of hybrid antibiotics. (Updated on 25-MAR-2003 to correct PN field.)

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or

Sequence 1208 BP;

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        in the biosynthesis of streptogramins, antibiotics active against Grampositive bacteria. The identification of the sequences encoding the enzymes involved in the biosynthetic pathway means that they can be isolated and manipulated. Mutant microorganisms in which a step in the streptogramin biosynthetic pathway is blocked can be cultured to produce streptogramin intermediates, which may later be converted to streptogramin derivatives. Recombinant cells may also be used for the bioconversion of streptogramins from one form to another or for the
                                                                                                                                                                                 DNA involved in streptogramin ar -conversion of streptogramin(s) derivs. or hybrid antibiotics.
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of streptogramins from one hybrid antibiotics. (Update
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30-MAR-2001; 2001US-0279709P
20-APR-2001; 2001US-0285214P
                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                           P-PSDB;
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The invention relates to identifying orthosomycin biosynthetic its fragment/gene cluster (ABZ66670-ABZ66813), comprising deter presence of a nucleic acid sequence coding for a polypeptide (ABP99362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene cluster. The method is useful for detectigene fragment or gene cluster.

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Matches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   presence of any organism that contains DNA for the production of orthosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new orthosomycin natural products, not produced by the organism
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Local Similarity 52.1%; Pred. No. 0.71;
hes 147; Conservative 0; Mismatches 129; Indels 6
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Sequence 16033, A	Sequence 16145, A	Sequence 4705, Ap	Sequence 4814, Ap	Sequence 11250, A	Sequence 26794, A	Sequence 1263, Ap	Sequence 5418, Ap	Sequence 1227, Ap	Sequence 915, App	Sequence 4601, Ap	Sequence 12884, A	Sequence 12577, A	Sequence 1029, Ap	Sequence 4319, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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APPLICANT: BLANC, Veronique
APPLICANT: THIBAUT, Denis
APPLICANT: THIBAUT, Denis
APPLICANT: BLANCHB, Francis
APPLICANT: BLANCHB, Francis
APPLICANT: BLANCHB, Francis
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: PAMECHON, Alain
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Best Local :
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TYPE: DNA
ORGANISM: Streptomyces
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Pred. No. 6.3e-21;
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; ORGANISM: Streptomyces pristinaespiralis
US-09-987-614A-4
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                                                                                                                                                          Sequence 1, Application Patent No. 6352839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.5%;
Best Local Similarity 69.8%;
Matches 183; Conservative
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                                                                                             APPLICANT: BLANC,
APPLICANT: THIBAU
APPLICANT: BAMAS-
APPLICANT: BLANCH
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APPLICANT: THIBAUT, Denis
APPLICANT: BAMAS-JACQUES, Nathalie
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CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PARTS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
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DEBUSSCHE, Laurent
FAMECHON, Alain
                                                                            BLANCHE, Fran
COUZET, Joel
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DEBUSSCHE, Laurent
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BAMAS-JACQUES, Nathalie
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COUZET, Joel
DUTRUC-ROSSET, Gilles
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Pred. No. 6.3e-21;
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; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-1
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                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09987614A Patent No. 6833382
 Matches 183;
                 Query Match
Best Local Similarity
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APPLICANT: THIBAU
APPLICANT: BAMAS-
APPLICANT: BLANCH
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Best Local Similarity
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CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                           APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/08/765,907
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DEBUSSCHE, Laurent
FAMECHON, Alain
                                                                                                                                                                                                                                                                                                                                                                                                  BLANCHE, Francouzer, Joel
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BAMAS-JACQUES, Nathalie
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                 Score 135.6; DB 4
Pred. No. 7.5e-21;
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Pred. No. 7.5e-21;
 Mismatches
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                                DB 4;
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14 ACGAGCTGCAGCGGCTGCGCGCGGAGCTCGACGCCCTCGACGGGACGCTCCTGGACACGG 73

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RESULT 6

US-09-252-991A-11423/c

; Sequence 11423, Application

; Patent No. 6551795

; GENERAL INFORMATION:
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US-09-252-991A-11493
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US-09-252-991A-11493
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Best Local S
Matches 138
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PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11493
LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARC J. Rubenfield et al.

AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 0.0029;
0; Mismatches 13
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Matches 138;
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11470
LENGTH: 1371
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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LENGTH: 1359
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 GGTCAGCCTGGTCAAGGACAGGGCCGCCCGCTACGCCGACCACGGCCTCGACGAATC
93 CGGTGTCCGCATCGCGCGGTACAAGTCCCGGCACGGCGTCCCCGATGATGCAGCCCGGCCG
                                                                                                           33 CGCGGAGCTCGACGCCCTCGACGGGACGCTCCTGGACACGGTGCGGCGCCGCATCGACCT
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                                                                                                                                                        Score 54.6; DB 4
Pred. No. 0.0031;
0; Mismatches 13
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Pred. No. 0.0031;
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DB 4; 118;

Length 15689; Indels

0;

Gaps

60 0

7805

240

7865 180 7925 120 7985

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Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2740
LENGTH: 1963
TYPE: DNA
Sequence 1129, Application US/09902540
PALENT NO. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Ge
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                 RESULT 9
US-09-902-540-1129/c
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US-09-902-540-2740
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Best Local
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US-08-403-852D-4
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1129
LENGTH: 15689
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
DATH COMPATON ATMED: 12 (16/16/20 66)
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE Finnegan, Henderson, Farabow,
ADDRESSEE: Finnegan, N.W., Suite 700
                                  APPLICATION NUMBER: US/00
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                        STATE: D.C.
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                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 17.4%;
Local Similarity 51.4%;
Les 125; Conservative
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    APPLICATION DATA:
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Jacques, Nathalie
Lacroix, Patricia
Thibaut, Denis
Zagorec, Monique
Debussche, Laurent
                                                                                                                                                                                                                                                            USA
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins,
VENTION: Coding For These Polypeptides Av
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Pred. No. 0.0048;
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Nucleotide Sequences nd Their Use

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RESULT 11
US-08-510-646B-4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                 APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Int
TITLE OF INVENTION: Biosynthesis Of
TITLE OF INVENTION: Coding For These
                                                                  NUMBER OF SEQUENCES: 4
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FILING DATE: 25-SEP-1992
ATTORNEY AGENT INFORMATION:
ADDRESSEE: Finnega
STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                  E: Finnegan, Henderson, Farabow, 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                               Blanche,
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Debussche, Laurent
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                                                                                             Polypeptides Involved In The Biosynthesis Of Streptogramins, Nucleotide Sequences Coding For These Polypeptides And Their Use
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Pred. No. 0.0042;
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                                                   Garrett & Dunner
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION NUMBER: US 08/403,852
PILLING DATE: 10-MAY-1995
PRIOR APPLICATION NUMBER: PCT/FR 93/009;
APPLICATION NUMBER: PCT/FR 93/009;
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9
FILING DATE: 25-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
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1100 CCATCTACGCCGCCACCGCCGCCTACGGCC
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                                                                                TGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGCGTCGAGGACCTGGTGATGA
                                                                                                                         GCCTGTTCGTCGAGACGTTCGGCACCGGCACCGTCGCCCAGGAGCGCATCGAGAAGGCCCA
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                                                          TCACCGAGGTCTTCGACCTGCGCCCCGCGGCCATCATCCGCGACCTCGACCTGCTGCCGCC
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50.0%;
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Pred. No. 0.0042;
0; Mismatches 13
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RESULT 12 US-09-231-818-4

Sequence 4, Application US/09231818 Patent No. 6171846 GENERAL INFORMATION:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE: 10-MAY-1995
FITH CATTON NUMBER: PCT/FR 93/00923
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                              NAME/KEY:
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GCCTGGTCAAGGACAGGGCCGCCGCCTACGCCGCCGACGACCACGGCCTCGACGAATCGTTCC 217
                                                   GCCTCGCCTCCCGCTGCGAGGTCCAGGTCGCCTACGCCATCGGCAAGGCCGAGCCGGTCG
                                                                                      TCCGCATCGCGCGGTACAAGTCCCGGCACGGCGTCCCGATGATGCAGCCCGGGCCGGGTCA 157
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25-SEP-1992
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                                                                                                                                                                                                            Score 54; DB 3; Length 1208; Pred. No. 0.0042;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                        135;
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US-09-635-359B-4
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                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: 09-Aug-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
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Zagorec, Monry.

Debussche, Laurent
De Crecy-Lagard, Valerie
De Crecy-Lagard, Valerie
Biosynthesis Of Streptogramins, Nuc
Coding For These Polypeptides And
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESSE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700
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                        FEATURE
                                                             ORIGINAL SOURCE:
                                                                             ANTI-SENSE: NO
                                                                                             HYPOTHETICAL: NO
                                                                                                                    MOLECULE TYPE: CDNA
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                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                             NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY:
                                                                                                                                                          STRANDEDNESS: double
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                                      ORGANISM: S.pristinaespiralis
                                                                                                                                    TOPOLOGY: linear
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US-08-403-852D-1
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Best Local
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                                                                                                                                                                                                                                         ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION:
                                                      FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                         FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                   APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/FR 93/00923
                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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NAME: MEYETS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03/
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    STREET: 1300 1 SUCTIV: Washington
                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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De Crecy-Lagard, Valerie
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                                                                              UMBER: FR 92/11441
25-SEP-1992
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Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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                 03806.0054-00000
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Pred. No. 0.
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Best Local Similarity
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APPLICANT: Blanc, Veronique
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                                                                                                                                                                                                                                              APPLICANT: Zagorec, APPLICANT: Debussche APPLICANT: De Crecy-TITLE OF INVENTION: TITLE OF INVENTION:
                                                         ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           SOPTWARE: PatentIn Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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CITY: Washington
                                                                                                                                    COUNTRY:
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TYPE: nucleic acid
STRANDEDNESS: double
 FILING DATE:
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Crouzet, Joel
Jacques, Nathalie
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Zagorec, Monique
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 03-AUG-1995
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4417 AGGTCGACCGTTCCGCCGCGTACGCGATGCGCTGGGTCGCCAAGAACGTCGTCGCCGCGG
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De Crecy-Lagard, Valerie
VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins,
VENTION: Coding For These Polypeptides Ar
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Pred. No. 0.0048;
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Version
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Search completed: October Job time: 59.8815 secs
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TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION UNMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
PILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                           312
296.4
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59.2
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312
                                                                                                                                                                Match
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                              7442561 seqs, 3452328358 residues
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                              Length DB ID
      312
3305
12391
3114
838
1009
1398
        14
19
20
18
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14
  US-10-472-587-3

US-10-126-927-68

US-10-126-927-67

US-10-437-963-48039

US-10-425-115-320

US-10-425-114-33332

US-10-156-761-1302
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                                                                                                                                                           Description
                  Sequence 3, Appli
Sequence 68, Appl
Sequence 67, Appl
Sequence 48039, A
Sequence 320, App
Sequence 33332, A
    Sequence
1302,
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ALIGNMENTS

RESULT 1 US-10-472-587-3

Sequence 3, Application US/10472587 Publication No. US20040214274A1

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GENERAL INFORMATION:

APPLICANT: YANNAI, Koji

APPLICANT: SIMIDA, Naomi

APPLICANT: WATANABE, Manabu

APPLICANT: WATANABE, Manabu

APPLICANT: MORIYA, Tatsuki

APPLICANT: MORIYA, Takeshi

TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods fo

TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods fo

TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods fo

TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods fo

TITLE OF INVENTION: Producing The Same And Novel Biosynthesis Genes

FILE REFERENCE: 2003-1302A/WMC/00144

CURRENT APPLICATION NUMBER: US/10/472,587

CURRENT PPLICATION NUMBER: US/20/472,587

CURRENT APPLICATION NUMBER: B2227/2001

PRIOR APPLICATION NUMBER: B2227/2001

PRIOR APPLICATION WIDSER: B2227/2001

PRIOR FILLING DATE: 2001-03-22

NUMBER OF SEQ ID NO 3

LENGTH: 312

TYPE: DNA

ORGANISM: Streptomyces venezuelae

FEATURE:
NAME/KEY: CDS

LOCATION: (1)...(309)

US-10-472-587-3

Query Match

100.0%; Score 312; DB 20; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.1e-75;
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APPLICANT: Meňí, Rýan A
APPLICANT: Pastrnak, Miro
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Aci
FILE REFERENCE: 54-000120Us
CURRENT APPLICATION UNMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
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                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-10-126-927-68
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US-10-126-927-68
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                                                                                                                                    Query Match
Best Local Similarity 98.4
Matches 311; Conservative
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SEQ ID NO 68
LENGTH: 3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 68, Application US/10126927 Publication No. US20030082575A1 GENERAL INFORMATION:
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APPLICANT:
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GTCCCGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGC
                                                                                                              ATGACCGAGCAGAACGAGCTGCA----GCGGCTGCGCGCGGAGCTCGACGCCCTCGACGG
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Liu, David R
Magliery, Thomas
Meggers, Eric L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schultz,
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98.4%;
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Pred. No. 7.6e-71;
0; Mismatches 1
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                                                                                                                                                                   DB 14; Length 3305;
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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; LENGTH: 12391
; TYPE: DNA
; ORGANISM: Plasmid
US-10-126-927-67
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US-10-126-927-67
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SEQ ID NO 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: US 60/285,030
PRIOR PILING DATE: 2001-04-19
PRIOR PILING DATE: 2001-04-19
PRIOR PILING DATE: 2001-04-19
PRIOR PILING DATE: 2002-02-06
NUMBER: OF SEQ ID NOS: 79
NUMBER: OF SEQ ID NOS: 79
NUMBER: OF SEQ ID NOS: 79
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APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
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                                                                                                                     CGCCCGCTACGCCGACCACGGCCTCGACGAATCGTTCCTGGTGAACCTCTACGACGT 236
                             GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCCGG
GATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGAGCCCG
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Liu, David R
Magliery, Thomas
Meggers, Eric L
Mehl, Ryan A
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Zhang, Zhiwen
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Santoro, Stephen
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97.9%;
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Pred. No. 2.6e-62;
0; Mismatches 2;
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2340
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
ITITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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US-10-437-963-48039
                                                                                                                                                                                                                                                                                        RESULT 5
US-10-425-115-320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_50752C
US-10-437-963-48039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21 (5221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NO 48039 LENGTH: 3114

TYPE: NNA
                                                                                                                                                                                                                                      Sequence 320, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                             NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 320
LENGTH: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48039, Application US/10437963 Publication No. US20040123343A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
ORGANISM: Zea FEATURE:
                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                         1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAAGGACTACGTCAAGGTCACCCTCATCGAGGCCAACGAGATCCTCCTCCTTCGAC 1032
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                                                                                                                                                                                                                                                                                                                                                                                        CGCGTCGAGGACCTGGTGATGAGCCGGGAGGAGCCTGACGGCCGAGGACCGGCG 308
                                                                                                                                                                                                                                                                                                                                                                                                                        GTCGGGCTGCGCCAGTACGCCACGGACCACCTCTCCAAGTACGGCGTGAACCTGGTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTTCAGCGGCGAGCTCAGCGACTTCATCACCCGCGACGTGCGGGAGAGGTACGCTCAC 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCGCCGCATCGACCTCGGTGTCCGCATCGCGCGTACAAGTCCCCGGCACGGCGTCCCG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAAGAAGAAGCGCCTCCTGCACTGCGTCGTCGTCGGCGGGGGTCCGACCGGGGTG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou, Yi
Cao, Yor
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                         GGCGTGGTGAAGGAGGTGAAGCCGAGGGAAGATCGAGCTGAGCGACGGAGCCG 1145
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Pred. No. 1.1e-06;
0; Mismatches 146;
                                                                                                                                                             and
                                                                                                                                                             Other Molecules
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US-10-425-114-33332
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Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                          Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                           Similarity
                  TGGCGCTGGGGTTCAGCTGGGCGCACCTCATCGGCGACATCCCG
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: US-10-425-114-33332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 33332
LENGTH: 1009
TYPE. NN
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                                                                                                                                       597 TCCGCGACGGCGCGCCCGGCAGGATCAGGCAGCTCTGCTACGACAAGGTGCTCGGCC
263 AGGACCTGGTGATGAGCCGGGAGAGCCTGACGGCCGAGGACCGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 GTCAGCCTGGTCAAGGACAGGGCCGCCCGCTACGC---CGCCGACCACGGCCTCGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 GCGGAGCTCGACGCCTCGACGGGACGCTCCTGGACACGGTGCGGCGCCGCATCGACCTC
                                                                       TCGACGAATCGTTCCTGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCG
                                                                                                                                                                               AGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGCCGCCGCTACGCCGCCGACCACGGCC
                                                                                                                                                                                                                            GCAACGACTGCGGCGTGCGCATCGTGGAGGCCAGGTGCGACCGCGACATGGCCGAGTGGA
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                                             CCGAGCTCTTCTTCTCGCCGCTGCTCTACGTCCAGATCACAAACTTCAAATGCGGTGGGC
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                                                                                                                                                                                                                                                                                                                                          18.5%;
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                                                                                                                                                                                                                                                                                                                  Score 57.6; DB 18
Pred. No. 3.7e-06;
0; Mismatches 104
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Pred. No. 1.4e-06;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                 DB 18;
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RESULT 7 US-10-156-761-1302

GENERAL INFORMATION:

Sequence 1302, Application US/10156761 Publication No. US20030119018A1

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RESULT 8
US-10-156-761-1/c
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; NAME/KEY: CDS
; LOCATION: (1)..(1398)
US-10-156-761-1302
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REFERENCE: 249-262
PILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1302
LENGTH: 1398
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                      Sequence 1, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                APPLICANT:
                                                                  APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
 OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                              309
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                                                                  ISHIKAWA, JUN
HORIKAWA, HIROSHI
              SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.6%; ilarity 48.8%; Conservative
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Pred. No. 1.8e-05;
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                                                                                 ; ORGANISM: Streptomyces mobaraensis US-10-107-431-76
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
                                                                                                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 76
LENCTH: 1458
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 76, Application US/10107431
Publication No. US20030224364A1
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  Matches 146;
                    Query Match
Best Local Similarity
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Best Local Similarity 48.8%;
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/107,431
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 282
                                                                                                                                                                                                                                                               APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: COMPOSITIONS A
TITLE OF INVENTION: BIOSYNTHETIC
FILE REFERENCE: 3001-7US
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OTHER INFORMATION: a, t,
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                    Score 54.8; DB 17; Pred. No. 2.1e-05;
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Pred. No. 1.2e-05;
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Mismatches
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                                     Length 1458;
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; TYPE: DNA
; ORGANISM: Streptomyces mobaraensis
US-10-107-431-277
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US-10-107-431-277/c
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US-10-156-761-1
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Best Local S
Matches 146
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APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANTON: EMMANUEL
TITLE OF INVENTION: ENCSYTHETIC LOCI
FILE REFERENCE: 3001-TUS
CURRENT APPLICATION NUMBER: US/10/107,431
CURRENT APPLICATION NUMBER: US/10/107,431
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 282
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 277
LENGTH: 43055
                                            Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 277, Application US/10107431 Publication No. US20030224364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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Pred. No. 1.8e-05;
0; Mismatches 152;
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NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c,
US-10-156-761-1
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSSI
APPLICANT: SAKAKI, YOSHIYI
APPLICANT: HATTORI, MASAHI
NUMBER OF SEQ ID NOS:
SEQ ID NO 3832
LENGTH: 1284
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3832, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.6%;
Best Local Similarity 50.0%;
Matches 137; Conservative
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SEQ ID NO 1
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APPLICANT:
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SHIBA, TADAYOSHI
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Pred. No. 1.4e
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RESULT 13
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Publication No. US20040229236A1
GENERAL INFORMATION:
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Best Local
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA

APPLICATION NUMBER: US/10/716,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Far
STREET: 1300 I Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200
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                                                                                                                                                                                                                                                                       FILING DATE: 20-Nov-2003 PRIOR APPLICATION DATA:
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COUNTRY: USA
ZIP: 20005-3315
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                                                                                                     APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403,852
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FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
                                                                                                                                                                                                       APPLICATION NUMBER: US 09/635,359 FILING DATE: 09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
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De Crecy-Lagard, Valerie
INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins,
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Crouzet, Joel
Jacques, Nathalie
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Thibaut, Denis
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Pred. No. 2.7e-05;
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iite 700
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RESULT 14
US-10-716-803-1
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Publication No. US20040229236A1
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Best Local Similarity
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FILING DATE: 25-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Arrigo, Salvatore J.
REGISTRATION NUMBER: 46,063
REFERENCE/DOCKET NUMBER: 03806.0054-04000
TELECOMMUNICATION INFORMATION:
             NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow,
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                           1100
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TELEFAX: (202) 408-44
RMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GCCGGGAGAGCCTGACGGCCGAGGACCGGC 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GCCTGGTCAAGGACAGGGCCGCCCGCTACGCCGCCGACCACGGCCTCGACGAATCGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                920 GCCTCGCCTCCCGCTGCGAGGTCCAGGTCGCCTACGCCATCGGCAAGGCCGAGCCGGTCG 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         860 AGGTCGACCGTTCCGCCGCGTACGCGATGCGCTGGGTCGCCAAGAACGTCGTCGCCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCGAGGTCTTCGACCTGCGCCCCGCGGCCATCATCCGCGACCTCGACCTGCTGCGGC 1099
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
CITY: Washington
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                                                       Thibaut, Denis
Thibaut, Denis
Zagorec, Monique
Zagorec, Monique
Debussche, Laurent
De Crecy-Lagard, Valerie
OF INVENTION: Polypeptides Involved In The
Blosynthesis Of Streptogramins, Nu
Ading For These Polypeptides And
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Lacroix, Patricia
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.4e-05;
ches 135;
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ORGANISM: S.pristinaespiralis SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-716-803-1
                                                             RESULT 15
US-10-107-431-112
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Sequence 112, Application US/10107431 Publication No. US20030224364A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/716,803
FILING DATE: 20-NOV-2003
PRIOR APPLICATION NUMBER: US/10/716,803
FRIOR APPLICATION NUMBER: US/10/716,803
PRIOR APPLICATION NUMBER: US/10/716,803
FILING DATE: 09-AUG-2000
FILING DATE: 09-AUG-2000
FILING DATE: 09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Arrigo, Salvatore J.
REGISTRATION NUMBER: 46,063
REFERENCE/DOCKET NUMBER: 03806.0054-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEPHONE: (202) 408-4400
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                                                                                                                                               4657
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                                                                                                                                            CCATCTACGCCGCCACCGCCCTACGGCC 4686
                                                                                                                                                                                                                                                                                                                                              GCCTGGTCAAGGACAGGGCCGCCCGCTACGCCGCCGACCACCGCCTCGACGAATCGTTCC 217
                                                                                                                                                                                                                                                                                                                                                                                      GCCTCGCCTCCCGCTGCGAGGTCCAGGTCGCCTACGCCATCGGCAAGGCCGAGCCGGTCG 4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTCGACCGTTCCGCCGCGTACGCGATGCGCTCGGCTCGCCAAGAACGTCGTCGCCGCGG
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                                                                                                                                                                                  GCCGGGAGAGCCTGACGCCGAGGACCGGC 307
                                                                                                                                                                                                                                                 TGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCGAGGACCTGGTGATGA 277
                                                                                                                                                                                                                                                                                                        GCCTGTTCGTCGAGACGTTCGGCACCGGCACCGTCGCCCAGGAGCGCATCGAGAAGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/231,818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-195
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                          TCACCGAGGTCTTCGACCTGCGCCCCGCGGCCATCATCCGCGACCTCGACCTGCTGCGGC 4656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 5392 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.3%;
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Pred. No. 3.2e-05;
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; APPLICANT: Farnet, Chris
; APPLICANT: Staffa, Alfredo
; APPLICANT: Staffa, Alfredo
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: BIOSYNTHETIC LOCI
; FILE REFERENCE: 3001-7US
; CURRENT APPLICATION NUMBER: US/10/107,431
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 112
; SOFTWARE: Patentin version 3.0
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Search completed: October Job time: 331.305 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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TYPE: DNA
                                                                     385
                                                                                                         268
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                                                                     CACGTGACGGACCCGGACACCCACCTGCGGGAGGCCCTCCGG
                                                                                                                                           AGCGCCCTGCCGGACGGCTCGTTCGACGGGATCCTCTC
                                                                                                                                                                               GAATCGTTCCTGGTGAACCTCTACGACGTGATCATCACGGAGATGTGCCGCGTCGAGGAC 267
                                                                                                                                                                                                                                                     GECCEGETCAGCCTEGTCAAGGACAGGECCGCCGCTACGCCCGCCGACCACGGCCTCGAC 207
                                                                                                                                                                                                                                                                                           GACTTCGGCGCGGCACGTCGCCTACCGCGGCCTGCTCCCGGGCGCCGAGCTGGAGACC
                                                                                                                                                                                                                                                                                                                             GACCTCGGTGTCCGCATCGCGCGCTACAAGTCCCCGGCACGGCGTCCCGATGATGCAGCCC
                                                                                                      CTGGTGATGAGCCGGGAGAGCCTGACGGCCGAGGACCGGCGG
                                                                                                                                                                                                                   GCCGAGATGCGCGGCGAGGACCTGACCGCCGACCACGAGCTGGACGCGGACGGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.1%;
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               2005, 09:57:04
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Pred. No. 4.5e-05
0; Mismatches 12'
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                                                                                                                                                                                                                                                                                                                                                                                                                                       129;
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                                                                       426
                                                                                                         309
                                                                                                                                             - CACCCAGGTCCTGGAG
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Result
No.
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                         Score
                                  seq length: 0
seq length: 2000000000

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312
1 atgaccgagcagaa
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Match Length
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gb_gss1:*
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GenCore version (c) 1993 - 2005
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CO8452094
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CK849616
CR456310
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CR550517
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AV688662
AV6809663
CK960904
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CN434658
AV610217
CK979444
CK981592
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CK849616
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CO877281
CN436828
CO882659
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CK981592
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CN434658
AV610217
                                                                                CR553143
                                                                                                                                                                        Description
                  AV666919
OSIFCC037
3 171374 BA
2 AV588862
                                             BE030008B
AV610217
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51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.8	51.8	52	52.6	52.6	53	53	53	53	53
16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.6	16.6	16.7	16.9	16.9	17.0	17.0	17.0	17.0	17.0
1016	856	825	817	810	792	754	753	730	568	557	1518	420	403	953	812	766	723	703	700	687
9	9	9	9	9	7	თ	σ	9	44	N	ø	μ.	7	9	ω	7	7	7	7	7
CC613501	CG221526	CG360167	CG217830	CG217836	CO894488	CA129331	CA129321	CG338179	AV610464	BE749820	CL966729	AJ475173	CN435245	CG447122	CC336291	CK848305	CK949352	CK971912	CK968936	CK961397
CC613501	CG221526	CG360167	CG217830	CG217836	C0894488	CA129331	CA129321	CG338179	AV610464	BE749820	CL966729	AJ475173	CN435245	CG447122	CC336291	CK848305	CK949352	CK971912	CK968936	CK961397
OGVAS74TV	OGXAT27TV	OGYCJ28TH	OG1CH30TH	OG1CH30TV	BovGen_22	SCRFLR203	SCRFLR203	осуврветн	AV610464	200869 MA	OBIFCC014	AJ475173	BE030011A	OGVHX58TV	OGIAH61TH	971049 BA	4074664 B	4087757 B	4084284 B	4102529 B

ALIGNMENTS

RESULT 1
CL973370
LOCUS
DEFINITION S 밁 Ś VERSION KEYWORDS ORIGIN FEATURES COMMENT REFERENCE SOURCE ACCESSION Query Match Best Local S Matches 147 TITLE ORGANISM AUTHORS JOURNAL source S Ma,L., Wangc,J., Chen,C., Liu,X.; Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,Ji, Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
L Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-8048159
Fax: 86-10-8048159 850 GAGGAAGAAGAAGCGCCTCCTGCACTGCGTCGTCGTCGGCGGGGGTCCGACCGGGGTG al Similarity 147; Conserv 76 CGGCGCCCCATCGACCTCGGTGTCCGCATCGCGCGTACAAGTCCCGGCACGGCGTCCCG 16 Oryza sativa (indica cultivar-gróup)
Oryza sativa (indica cultivar-gróup)
Cyza sativa (indica cultivar-gróup)
Eukaryota; Viridiplantae; Streptóphyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1686) CL973370
CL973370
CL973370
CLSTC024109 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. Class: exon-trapped Rice genomic sequence. CL973370.1 GI:52401267 Email: chenchen@genomics.org GAGCTGCAGCGGCTGCGCGGAGCTCGACGCCCTCGACGGGACGCTCCTGGACACGGTG 19.0%; ilarity 50.2%; Conservative /organism="Oryza sativa (indica cultivar-group)"
/mol type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences Location/Qualifiers .1686 0; Score 59.4; DB Pred. No. 0.006; 0; Mismatches 1 G G 146; Indels 9; Length 1686; GSS 21-SEP-2004 0 Gaps Cao, M., and 135 909 75 0

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SOURCE
ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewin,H.A., Renard,J.P., Y
Hue,I., Tian,X.C., Liu,L.
Bovine embryonic ESTs
Unpublished (2004)
Contact: Harris Lewin
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CN434658.1
EST.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trimming: Cross match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length with average PHRED score > 20. REPEAT IN THE SEQUENCE Low complexity STRAND (+) ELEMENT GC_rich LOCATION [350,383].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funding for embryonic EST sequencing was provided by USDA ARS contract No. 58-1275-2-020 to H. A. Lewin. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Animal Sciences
University of Illinois at Urbana-Champaign
206 Edward R. Madigan Laboratory, 1201 W. Gregory Dr.,
                                                                                                                                                                                                                                                                                                                                                               Insert Length: 422 Std Er
Plate: BE030008B10 row: H
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extraembryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: h-lewin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTGTGGAATTGTGAGCGGATAACAA
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217 244 5617
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/mote="Vector: pGEMZÉNI(+); Site 1: ECORI; Site 2: NotI; /note="Vector: pGEMZÉNI(+); Site 1: ECORI; Site 2: NotI; The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez, W.M. Keck Center, University of Illinois Urbana-Champaign and S. Degrelle,
                                                                                                                                         /organism="Bos taurus"
/mol_type="mRNA"
/db xref="taxon:9913"
/clone="BE03000BB10H11"
/clone="BE03000BB10H11"
/tissue type="embryoic tissue (day 14 to 25) Normalized subtracted library"
                                                                                                /clone_lib="BE03 Normalized and Subtracted bovine
                                                                                                                           lab_host="DH10B"
                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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BE03 Normalized and Subtracted bovine embryonic
tissue Bos taurus cDNA clone BE030008B10H11 5',
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                                                                                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
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MEDLINE
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                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                     PUBMED
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Animal Genetics Division Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, Fuku Tel: 81-248-25-5641 Fax: 81-248-25-5725

Fukushima

961-8061,

Single pass sequencing. This clone was obtained

obtained from a polyA-deleted cDNA library

Email: kazusugi@cocoa.ocn.ne

21570554 11713328

Nucleic Acids Res. 29 (22), E108 (2001)

bovine ESTs

Establishment of a high throughput EST sequencing system poly(A) tail-removed cDNA libraries and determination of

Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,

Suzuki, H.,

Aso, H.

of 36,000

and Sugimoto,Y.

Bovinae; Bos.

(bases 1 to 653)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;

Euteleostomi;

mRNA sequence. AV610217 AV610217.1 GI

GI:9745887

Bos taurus (cow)

Contact: Yoshikazu Sugimoto

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RESULT 3
AV610217/c
     DEFINITION
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AV610217
AV610217 Bos taurus lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 France, as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. This clone is from library BEO3, a normalized library of embryonic tissues subtracted with 7800 known placental EST sequences. The double stranded cDNA was size selected (more than 450 bp), adaptored with EcoRI adaptors at both ends and then digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested gGEM11Ef(+) phagemid vector. Insert size was between 450-2200 bp. Sequencing was done from the 5' end of the clone. Tagged oligo-dT was used to identify the source of the ESTs where possible. (A18)TGCGT = extraembryonic tissue, (A18)TGCGT= 36-day old fetus; (A18)TGCGA = 64-day old fetus (organs); (A18)TGCGA = 64-day old fetus (organs)
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  653 bp
fetus Bos
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No. 0.071;
  mRNA linear I
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JOURNAL COMMENT
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AUTHORS
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                      TITLE
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                                          Single pass sequencing. Bases called and to .000925 using options -trim_alt " -trim_fby cross_match using options -minmatch 12 plate: 39 row: H column: 08 seq_primer: CCCAGTCACGACGTTGTAAAACG
                                                                                                                                                                Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Edlg. 200 Rm2A BARC-East, Beltsville, W
Tel: 3015048416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
CK979444
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                                                                                                                                                                                                                                                                                   1 (bases 1 to 678)
Sonstegard, T.S., Van Tassell, C.P., Matukumal
G.P., Bosak, S., Rubenfield, M. and Gasbarre,
Production of EST from cDNA libraries derived
                                                                                                      Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK979444 678 bp mRNA linear ES: 4110945 BARC 9BOV Bos taurus cDNA clone 9BOV39_H08 5',
                                                                                                                                                                                                                                                                   activated bovine gut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CK979444.1 GI:45497424
                                                                                                                                                    Fax: 3015048414
                                                                                                                                                                                                                                                   Unpublished
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                               quality sequence stop: 678.
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="lung"
/dev_stage="fetus"
/lab_host="DH10B"
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51.0%;
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Pred. No. 0.069;
0; Mismatches 1
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Gasbarre, L.C.
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CK981592
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immuserivated bovine gut
Unpublished (2004)
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt " -trim fasta. Vector iden by cross match using options -minmatch 12 -minscore 12 plate: 43 row: J column: 12
                                                                                                                                       Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, I
                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eurheria: Cetartiodactyla, Ruminantia, Pec
                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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                                                                                 Email: tads@anri.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK981592.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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                                                                                                      Fax: 3015048414
                                                                                                                         Tel: 3015048416
                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
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/dev_stage="Multiple"
/lab_nost==DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
/site_2: Not1; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
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/mol_type="mRNA"
/strain="Holstein"
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Pred. No. 0.069;
0; Mismatches 124;
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RESULT 6
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Best Local Sim:
Matches 129;
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                                                                                                                          G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C. Production of EST from cDNA libraries derived from immunologically Unpublished (2004)
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                                                                       Contact: Tad S. Sonstegard
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Hdlg. 200 Rm2A BARC-East, Beltsville, N
                                                                                                                                                                                                                                                                                                                                                               CK981688
4113939 BARC 9BOV
   Single pass sequencing. 0.000925 using options -
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                        EST.
Bos taurus (cow)
                             Email: tads@anri.barc.usda.gov
                                              Fax: 3015048414
                                                                                                                                                                                                                                                                           Bos taurus
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Location/Qualifiers
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/clone="9BOV43_J12"
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51.0%;
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_host="DH10B T1 phage resistant"
ne_lib="BARC 9BOV"
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9BOV43_E02 5', mRNA
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TITLE
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                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                   FOCUS
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                                                                                                      JOURNAL
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
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                                                                                                                                                                                                                                                                                           1 (bases 1 to 712)
Hennig,S., Janitz,M., Herwig,R.
Generation, annotation, evolutio
integration of 14969 cattle EST
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 bp mF
BovGen_05606 normal cattle brain Bos
RZPDP105601856Q 3', mRNA sequence.
CO877281
CO877281.1 GI:51807196
EST
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                                        Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                                                                                                               Contact: Hennig S
laboraty 123, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Email: hennig@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAGGTCATCT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terrectanter to the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACGGAGATGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCGCGCATGATGATGCAGTCGGGGCGCAAAGGAGCCGACATCATGTACAAGGGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGATCGCGCAGACCGTGACGGCCGTGGCGGGCGTCTCCTACCCCTTCGACACCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Multiple"
/lab_host="DH10B Tl phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
/note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
Site_2: Notl; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exposure to Ostertagia ostertagi was initiated at 15 of age. fundic and pyloric abomasum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="9BOV43_E02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%;
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                                                                                                                                                                                                                                                                                                                                                                                     Herwig,R. and Williams,J
n, evolutionary analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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).069;
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s cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
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RESULT 8
CN436828
COMMENT
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                                                                                                          REFERENCE
                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                           ACCESSION
                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                     AUTHORS
                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTCCTGGACACGGTGCGGCGCCCCATCGACCTCGGTGTCCGCATCGCGCGCTACAAGTCC
                                                                                                                                                                                                                                                                                                                            CN436828 714 bp mRNA linear EST 07-JUL-20 BE04010B1F12 BE04 Normalized and Subtracted bovine embryonic and extraembryonic tissue Bos taurus cDNA clone BE04010B1F12 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲
                                                                                                                                                                                                                                                               sequence.
CN436828
CN436828.1 GI:46416092
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                  Bovine embryonic ESTs
Unpublished (2004)
                                                          1 (bases 1 to 714)
Lewin, H.A., Renard, J.P.,
Hue, I., Tian, X.C., Liu, L
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                               TSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP) 5'-seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq Seq primer: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP).
                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomforschung GmbH (http://www.rzpd.de).
                                                                                                                               Bovinae; Bos.
                                                                                                                                                                                                                     Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGACCGAGCAGAACGAGCTGCAGCGGCTGCGCGCGGAGCTCGACGCCCTCGACGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCACGGAGATGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGACTGCTGGCGGAAGATCCTCAAGGACGAGGGCGGCAAGGCCTTCTTCAAGGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAAGGTCATCT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTCCAACGTTCTGCGCGGCATGGGCGCGCGCCTTCGTGCTGGTCCTCTACGACGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: brain; Vector: pSport1; Site 1: Not1; Site 2: Sal1; Random primed and directionally cloned in pSport1 vector using Not1 (5'-pGACTAGTTCTAGATCGCGAGCGCCCC (T)15-3' and Sal1 5'-TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RZPDp1056J1856Q"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="brain tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.5%;
51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _stage="adult brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lib="normal cattle brain"
                                                            Liu, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.6;
Pred. No. 0.
                                                              Yang, X.J., F. and Everts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                              Hernandez,A.,
s,R.E.
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                                                                                                                                                                                                                                                                                                   1 ATGACCGAGCAGAACGAGCTGCAGCGGCTGCGCGCGGAGCTCGACGCCCTCGACGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 714 Std Error: 0.00 Plate: BE04010B1 row: F column: 12
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University of Illinois at Urbana-Champaign
206 Edward R. Madigan Laboratory, 1201 W. Gregory Dr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: CCAGTCACGACGTTGTAAAACGAC (M13 NIA-F)
BACKWARD: GTGTGGAATTGTGAGCGGATAACAA (M13 NIA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: h-lewin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 217 333 5998
Fax: 217 244 5617
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                                                     CGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGGCCGCC 180
                                                                                                                  CGGCGGCGCATGATGATGCAGTCGGGGCGCAAAGGAGCCGACATCATGTACAAGGGCACC
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Instead of the constructed, normalized and subtracted by Dr. A. Hernandez, M.M. Keck Center, University of Illinois Urbana-Champaign and S. Degrelle, BDR, Institut National de la Recherche Agronomique, France, as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research (9): 791-806. This clone is from library BBO4, a normalized library of embryonic tissues subtracted with 7800 known placental EST sequences and 5000 clones from the BBO3 library. The double stranded cDNA was size selected (more than 450 bp), adaptored with BCORI adaptors at both ends and then digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEMI1Zf(1) phagemid vector. Insert size was between 450-2200 bp. Sequencing was done from the 5' end of the clone. Tagged oligo-dT was used to identify the source of the ESTs where possible. (A18)TGCGT = extrambryonic tissue; (A18)TGCGT = 36-day old fetus; (A18)TCGGA = 64-day old fetus (organs); (A18)TCGGA =
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embryonic and extraembryonic tissue"
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extra-embryonic tissue (day 14 to 25) Normalized and twice
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Pred. No. 0.069;
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The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONFP cluster was selected for sequencing. cDNA clones and
filters are distributed via Deutsches Ressourcenzentrum fuer
Genomforschung GmbH (http://www.rzpd.de).
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Hennig,S., Janitz,M., Herwig,R. and Williams,J.
Generation, annotation, evolutionary analysis and database
integration of 14969 cattle EST clusters
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 bp mRNA linear ES' BovGen 10984 normal cattle brain Bos taurus cDNA clone RZPDp1056D1724Q 5', mRNA sequence.
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Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
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laboraty 123, dept.Lehrach
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EST.
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CGGCACGGCGTCCCGATGATGCAGCCCGGCCGGGTCAGCCTGGTCAAGGACAGGCCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/note="Organ: brain; Vector: pSportl; Site 1: NotI;
Site_2: SalI; Random primed and directionally cloned in
pSportl vector using NotI
(5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and SalI 5'-
TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="brain tissue"
/dev_stage="adult brain"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.5%;
51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.6; DB Pred. No. 0.069 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                         124; Indels
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CR552094
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by funds dedicated to Funding for EST sequencing was provided by funds dedicated to J.P.RENNARD (BBR, Inra). Funding for construction and subtraction of the cDNA library was provided by USDA ARS contract No 58-1275-2-020 to H. A. Lewin The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez (W.M. Keck Center, University of Illinois Urbana-Champaign) and S. Degrelle (BBR, Inra) as described in Bonaldo et al. (1996), Genome Research 6, 791-806, BE03 library is a normalized library of embryohic tissues subtracted with 7800 known EST sequences. The double-stranded cDNA was size selected (+450 bp), adaptored with ECORI abaptors at both ends and digested with Not1. The cDNA was then direttionally cloned into EcoRI-Not1 digested pEMNIZE(+) phagemid vector. Insert size was between 450-2200 bp. Sequence cleaned of vector, adaptator and repetitions. Of this geometre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CGCTACGCCGCCGACGGCCTCGACGAATCGTTCCTGGTGAACCTCTACGACGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Embryonic ESTs (bcaz)
Unpublished (2004)
Contact: Renard JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR552094
CR552094 Normalized and extraembryonic tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renard, J.P., Lewin, H.A., Everts, R.E. and Hue, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR552094.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 740)
                                                                                                    /clone lib="Normalized and Subtracted bovine embryonic and extraembryonic tissues (bcaz)"
/note="Vector: pGEMZf11; Tagged oligo-dT was used to identify the origin of the ESTs where possible. (A18)TGCGT = extraembryonic tissue; (A18)TCGGT = 36-day oldfetus; (A18)TGCGA = 64-day old fetus (organs); (A18)TCGGA = 64-day old fetus (body)"
                                                                                                                                                                                                                                                                                                                /tissue type="embryo (day 36 and day 64), extra-embryonic tissue (day 14 to 25)"
                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    clone="bcaz0007a.j.09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Bos taurus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:50247004
17.5%;
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Score 54.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang, J.,
6; DB 7;
0.069;
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                           Length
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Matches 129;

Conservative

Mismatches

124;

0

Gaps

0

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REFERENCE
AUTHORS
TITLE
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CO874118
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
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CO874118.1 GI:51803967
EST.
Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hennig,S., Janitz,M., Herwig,R. and Williams,J. Generation, annotation, evolutionary analysis a integration of 1496 cattle EST clusters Unpublished (2004)
Contact: Hennig S
                                                                                                                                                                                                                                                                                                                                                                                                                                  The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with battery of 200 8mer oligonucleotides are grouped into clusters. On clone per ONFP cluster was selected for sequencing. CDNA clones an filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (http://www.rzpd.de).
                                                                                                                                                                                                                                                                                                                                                BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' (M13RSP).
                                                                                                                                                                                                                                                                                                                                                                         FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP) 5'-seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-sei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hennig@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ihmestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
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Max-Planck-Institut fuer Molekulare Genetik
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BovGen_02443 normal
RZPDp1056J1856Q 5',
                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 745)
                             /tissue type="brain tissue"
/dev_stage="adult brain"
/clone lib="normal cattle brain"
/note="Organ: brain; Vector: pSport1; Site_1: NotI;
Site_2: Sall; Random primed and directionally cloned in
pSport1 vector using NotI
[5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and Sall 5'-
                                                                                                                                                                                                sex="female"
                                                                                                                                                                                                                clone="RZPDp1056J1856Q"
                                                                                                                                                                                                                                                           mol_type="mRNA"
                                                                                                                                                                                                                                                                                  organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                    xref="taxon:9913"
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                adapters (Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                       (M13FSP)
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VERSION
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DEFINITION
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Best Local Similarity
                                                                                                                                                      source
                                                                                                                                                                                                               Funding for EST sequencing was provided by funds dedicated to J.P.RENARD (BDR, Inra). Funding for construction and subtraction of the cDNA library was provided by USDA ARS contract No 58-1275-2-020 to H. A. Lewin The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez (W.M. Keck Center, University of Illinois Urbana-Champaign) and S. Degrelle (BDR, Inra) as described in Bonaldo et al.(1996), Genome Research 6, 791-806. BE03 library is a normalized library of embryonic tissues subtracted with 7800 known EST sequences. The double-stranded cDNA was size selected (>450 bp), adaptored with EcoRI adaptors at both ends and digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEM11Zf(+) phagemid vector. Insert size was between 450-2200 bp. Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renard, J.P., Lewin, H.A., Yang, J., Everts, R.E. and Hue, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: renard@jouy.inra.fr
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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/clone="bcaz0010a.m.23"
/tissue_type="embryo (day
tissue (day 14 to 25)"
                                                                        /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                       organism="Bos"
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Pred. No. 0.069;
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                       and day 64), extra-embryonic
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Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by funds dedicated to
J.P.RENARD (BDR, Inra). Funding for construction and subtraction of
the cDNA library was provided by USDA ARS contract No 58-1275-2-020
to H. A. Lewin The cDNA library was constructed, normalized and
subtracted by Dr. A. Hernandez (W.M. Keck Center, University of
Illinois Urbana-Champaign) and S. Degrelle (BDR, Inra) as described
in Bonaldo et al.(1996), Genome Research 6, 791-806, BE03 library
is a normalized library of embryonic tissues subtracted with 7800
known EST sequences. The double-stranded cDNA was size selected
(*450 bp), adaptored with EcoRI adaptors at both ends and digested
with NotI. The cDNA was then directionally cloned into EcoRI-NotI
digested pGEM11Zf(+) phagemid vector. Insert size was between
450-2200 bp. Sequence cleaned of vector, adaptator and repetitions.
Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram
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No. 0.069;
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.B.
Connor, E. B., Cho, J., Sultana, R., Shade, L., Wray, J.E.,
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGACCGAGCAGAACGAGCTGCAGCGGCTGCGCGCGGAGCTCGACGCCCCTCGACGGGACG
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
                                                                                       Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                          Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                      the Bos taurus gene index
Mamm. Genome 13 (7), 373-379
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/note="Vector: pgEMRZf11; Tagged oligo-dT was used to identify the origin of the ESTs where possible. (A18)TC extraembryonic tissue; (A18)TCGGT = 36-day oldfetus; (A18)TCGGA = 64-day old fetus (organs); (A18)TCGGA = 64-day old fetus (body)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="bcaz0007a.p.12"
/tissue_type="embryo (day
tissue_(day_14_to_25)"
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/db_xref="taxon:9913"
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CR456310.1
EST.
Domaine de Vilvert 78350 Jouy en Josas, FRANCE Email: renard@jouy.inra.fr
Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by a Genanimal contract from FNS- Ministere de la Recherche (INRA, Num: A02085). Funding for construction and subtraction of the cDNA library was provided by USDA ARS contract No. 58-1275- 2-020 to H. A. Lewin The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez (W.M. Keck Center, University of Illinois Urbana-Champaign) and S. Degrelle (BDR, Inra) as described in
                                                                                                                                                                                              Contact:
Biologie
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR456310 Normalized and extraembryonic tissues 5', mRNA sequence.
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Everts, R.E. and Hue, I.
Embryonic ESTs (bcaz)
Unpublished (2004)
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Seq primer: GTAATACGAO
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/lab_host="DH10B"
/clone_lib="BARC_5BOV"
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/mol_type="mRNA"
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Pred. No. 0.068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGACCGAGCAGAACGAGCTGCAGCGGCTGCGCGGAGCTCGACGCCCTCGACGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo et al. (1996), Genome Research 6, 791-806. BE04 library is a normalized library of embryonic tissues subtracted with 7800 known EST sequences. The double- stranded cDNA was size selected (>450 bp), adaptored with EcoRI adaptors at both ends and digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEM12f(+) phagemid vector. Insert size was between 450-2200 bp. Sequence cleaned of vector, adaptator and repetitions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of this sequence.
AAGAAGGTCATCT
                                               ATCACGGAGATGT
                                                                                            TGGTCCAACGTTCTGCGCGCGCATGGGCGCGCGCCTTCGTGCTGGTCCTCTACGACGAGCTC
                                                                                                                                                                                                                                                                                      CGGCGGCGCATGATGATGCAGTCGGGGCGCAAAGGAGCCGACATCATGTACAAGGGCACC
                                                                                                                                                                                                                                                                                                                                        CTCCTGGACACGGTGCGGCGCCGCATCGACCTCGGTGTCCGCATCGCGCGGTACAAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="embryo (day 36 and day 64), extra-embryonic tissue [day 14 to 25)"
/lab host="PH10B"
/clone lib="Normalized and Subtracted bovine embryonic and extraembryonic tissues (bcaz)"
/note="Vector: pGEMZf11; Tagged oligo-dT was used to identify the origin of the ESTs where possible. (A18)TGCGT = extraembryonic tissue, (A18)TGCGT = 36-day oldfetus; (A18)TGCGA = 64-day old fetus (organs); (A18)TCGGA =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="bcaz0018e.n.09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9913"
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51.0%;
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Pred. No. 0.068;
0; Mismatches 1
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Result
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-Q=/cgn2_1/USPTO_spool h/US10089514/runat_04102005_105744_8033/app_query.fasta_1.1621
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LCCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MXXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-MODEL=frame+_p2n.model .
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514
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2: gb_htg:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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BD093915 Transform
AB116234 Streptomy
AF262220 Streptomy
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BD178314
LOCUS
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ontinuation (11	BX93639	_	-	9	100	43	
ntinual	BX936398_0	_	_	9.	100	42	
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nuati	000096	_	_	9.	101	36	
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7 Sequence		6	3659	9	101	29	
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Sequence	108481	σ	1253		101	27	
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1871 Photorha	BX57187	μ	4	·	2	10	()
417 Streptomy	SPU604	μ	4740	9	ū	9	
198353 Sequenc	AR19835	σ,	2888	9	σ.	8	
323 Sequence	A48323	σ	2888	9	s	7	
198355 Seque	AR1	σ,	387	49.8	256	o i	
	A483	6	387	9	s	σ	

ALIGNMENT

DEPINITION
Transformant producing PF1022 substance and process for producing DEFINITION
Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene.

BD178314
VERSION
BD178314
COMMENT
TITLE
Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene.

BD178314
COMMENT
Sureptomyces venezuelae
DOURNAL
AUTHORS
Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene
Patent: WO 02077244-A 2 03-OCT-2002;
WEIJI SEIKA KAISHA LTD, KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE,
TATSUKI MORIYA, TAKESHI MURAKAMI
OS Streptomyces venezuelae
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002782
PF 22-MAR-2001 JP 01P 082227
PF 22-MAR-2001 JP 01P 082227
PF 22-MAR-2001 JP 01P 082227
PF 22-MAR-2001 JP 01P 082227
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PF 22-MAR-2001 JP 01P 08227
PF 22-MAR-2001 JP 01P 08227
PF 22-M

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RESULT 2
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ORGANISM
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Best Local Similarity:
Query Match:
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Transformants that produce secondary metabolites modified by a functional group(s) and novel biosynthesis genes
Patent: WO 0123542-A 2 05-APR-2001;
MEIJI SEIKA KAISHA LTD, KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA,
MANABU WATANABE, KOICHI MIYAMOTO, NAOKI MIDO, TAKESHI MURAKAMI
OS Streptomyces venezuelae
PN WO 0123542-A/2
PD 05-APR-2001
PF 29-SEP-2000 WO 2000JP006783
PR 29-SEP-1900 WO 2000JP006783
PR 29-SEP-1900 WO 2000JP006783
PR 29-SEP-1900 WO 2000JP006783
PR 29-SEP-1900 WO CAKKURA, SHOHEI YASUDA, MANABU WATANABE, KO
                                                                                                                                                                    BD093915
BD093915.1 GI:22639503
WO 0123542-A/2.
WO 0123542-A/2.
Streptomyces venezuelae
Streptomyces venezuelae
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                   AspArgArg 103
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nai,K., Okakura,K., Yasuda,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
Key
CDS
29-SEP-2000 WO 2000JP006783
29-SEP-1999 JP 99P 276314
KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA, MANABU WATANABE, KOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transformant producing PF1022 producing the same and novel biosynthetic gene
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Location/Qualifiers
Location/Qualifiers
1. 312
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/mol_type="genomic DNA"
/db_xref="taxon:54571"
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Matches:
Conservative:
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2 (bases 1 to 5251)
Yanai,K., Sumida,N.,
Murakami,T.
Direct Submission
                                                                                                                                                                                                                               Streptomyces venezuelae
Streptomyces venezuelae
Streptomyces venezuelae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                   AB116234 5251 bp DNA linear BCT 03-JUI Streptomyces venezuelae paph, papb, ORFIV genes for 4-amino-4-deoxychorismate synthase, 4-amino-4-deoxyprephenate dehydrogenase, 4-amino-4-deoxychorismate mutase, hypothetical
                                                                                 Nat. Biotechnol.
15184904
                                                                                                                                           Para-position derivatives of engineered with Streptomyces
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AB116234
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C12N15/09,C12N5/10,C12P21/02,C07K11/00//(C12P21/02,C12R1:645)
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                                         Okakura, K., Moriya, T.,
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AMVFGIPEAAAGFGPLARARHKDAYLKRIDECLKEIRNGESYEICLTNNVTAPTEAT
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/db xref="taxon:54571"
651. 2711
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2708. .3676
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LGGSPEVYGDIQRSNPRAASARRALAEALRSFAALVGDDPDRADAPGRADAPGHPGGC
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EVVDLMNGMALVARGAALLVQGGDCAERFHEAVPDLVRRKVDNLQGLAAIMRAGSGLP
AVALGRIAGQYGKPRSS PFBTEESGAGRKMBS YCGDAVNEPBETBEPARTPEPRILLTA
YTCSQIVLDEIRRSMSGRPVLERVYTSHELLLLLP KERPLVREGAHTYSGSAHFGWIG
ERTRREDGAHVALAQAVHNPVGVKLGFTVSPEDAVALSRSLNPEGVPGRLTFIVRFGA
KEVDELLPPVVRAVARHGAPVVMLCDPMHGNGLKLAGHKTRLIEPMRAETAAFVRTLR
EHGQWPAGLHLELTPDPVTECVSELDRPPRFTDYRSTCDPRLNPEQSADMVTHFLSLL
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                                         Submitted (01-MAY-2000) Biology, Dal
St, Halifax, NS B3H 4J1, Canada
3 (Dases 1 to 14159)
He,J., Magarvey,N.A. and Vining,L.C.
                                                                                                                                                                             He,J., Magarvey,N., Piraee,M. and Vining,L.C.
The gene cluster for chloramphenicol biosynthesis in Streptomyces
venezuelae ISP5230 includes novel shikimate pathway homologues and
a monomodular non-ribosomal peptide synthetase gene
Microbiology 147 (Pt 10), 2817-2829 (2001)
                                                                                                                                                                                                                                                                                                                                                                    Streptomyces venezuelae chloramphenicol biosynthetic gene cluster, partial sequence.
AF262220
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Submitted (05-JUN-2001) Biology, St, Halifax, NS B3H 4J1, Canada
                                                                                                    He,J., Magarvey,N.A. and Vining,L.C. Direct Submission
                                                                                                                                                                                                                                                                                       Streptomyces venezuelae
Bacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                         Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 14159)
                                                                                                                                                                                                                                                                                                                       Streptomyces venezuelae
                              Direct Submission
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FEATURES
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On Jun 5, 2001 this sequence version replaced gi:10716943.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AECPAGERVLYNGEHTAEAVWALLAMISHAVHTENNOGLEPADREEFARVADAALLY
CFEREALURGEKAGLEALYAGDVGMPTDPAPAEAGTADEPARERVAYSI FTSGSTGD
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PSAAHEEVHUDILGRLLGTPPDTPAGDRAPERTTGTTSRGFERRRPRADTALTGTEP"
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5043. .5075
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                                                                                                4893.
                                                                                                                4833. .4853
/note="Region:
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4494. .4538
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4089. .4100
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NADH binding site"
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AUTHORS
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Best Local Similarity:
Query Match:
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Blanc, V., Thibaut, D., Bama,
Barriere, J., Debussche, L.,
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A48325
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                    (1-387)
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US-10-089-514-4 (1-103) x AF262220 (1-14159)
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                                                                                                                                                                                                                                                                                                                                 Dutruc-Rosset, G.
STREPTOGRAMINES AND METHOD FOR PREPARING
PATENT: WO 9601901-A 3 25-JAN-1996;
RHONE POULENC RORER SA (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces pristinaespiralis Bacteria; Actinobacteria; Actinomycetales;
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                                                                                                                                                                                                                                                  publication AU 2891295 960209
publication FR 2722210 960112
Location/Qualifiers
1. .387
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from Patent WO9601901.
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e,L., Famechon,A., Paris,J. an
                     Conservative: Mismatches: Indels:
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1 (bases 1 to 387)

Blanc, V., Thibaut, D., Bamas-Jacques, N., Bl.
Barriere, J.-C., Debussche, L., Famechon, A.,
Dutruc-Rosset, G.
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Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F., Crouzet, J., Barriere, J.-C., Debussche, L., Famechon, A., Paris, J.-M. and Dutruc-Rosset, G.
                                          Streptogramins for preparing same b Patent: US 6352839-A 1 05-MAR-2002;
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Other publication AU 2891295 960209
Other publication FR 2722210 960112.
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                                                                                                                                                                                                                                                                                                                                                                                          Identification and analysis of genes from Streptomyces pristinaespiralis encoding enzymes involved in the biosynthesis the 4-dimethylamino-L-phenylalanine precursor of pristinamycin I Mol. Microbiol. 23 (2), 191-202 (1997)
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Blanc, V., Gil, P., Bamas-Jacques, N., Lorenzon, S., Zagorec, M., Schleuniger, J., Bisch, D., Blanche, F., Debussche, L., Crouzet, J.
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Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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68. .2227
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                                                                                                                                                              Location/Qualifiers
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complement (2486. .3376)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genrue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: lfrangeu@pasteur.fr, fkunst@pasteur.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duchaud, E., Rusniok, C., Frangeul, L., Buchrieser, C., Taouri Bocs, S., Boursaux-Eude, C., Chandler, M., Dassa, E., Derose, I Derzelle, S., Freyssinet, G., Gaudriault, S., Givaudan, A., Gledigue, C., Lanois, A., Powell, K., Siguier, P., Wingate, V., Zouine, M., Boemare, N., Danchin, A. and Kunst, F.
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BX571871 BX470251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of the entomapathogenic bacterium
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Photorhabdus luminescens subsp. laumondii TTO1
Bacteria; Proteobacteria; Gammaproteobacteria;
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VGDTADPEGF I RQLAEQFPKYEEVLMT I AQKLQHKGHQEGLKEGLQKCQDAREEGLQE
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US-10-089-514-4 (1-103)
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SCIENTIFIQUE (CNRS) (
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Danchin, A. and Buchrieser, C.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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649980~seq 10791: 600001 to 696798"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphyromonas gingivalis W83
Porphyromonas gingivalis W83
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete Genome Sequence of the Oral Pathogenic Bacterium Porphyromonas gingivalis Strain W83
J. Bacteriol. 185 (18), 5591-5601 (2003)
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AE017175 AE015924
AE017175.1 GI:34396931
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                                                                                                                                                                                                                                                                                                                                                                       ubmitted (29-OCT-2002) The Institute for sdical Center Dr., Rockville, MD 20850, UD Cocation/Qualifiers
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complement(3939. 5105).

/locus_tag="PG0851"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="Mickhihihiktttpakrtssmtsksiknkiasfemgkvfrled
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EMLRLLDCLKWIKKIPDTTTDKSYILLKKKVNEYAKEEQKQLVELALKYSPLTRALLG
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/locus_tag="PG0849"
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SLSSK1RHFYDLNALLAIKELEEYVCSEEFVNDVETLVKHDQEAFDEPAGWKDLKDLN
QSPLVMDFDKLMDSLAPKYEENLGA1AYRE1PSSETIKASFLKILKSLRVIDLTKE"
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I KEAKEDLAG FEKR VERDAEGLPI INKLITIKGVEGSTDI KYTARLQBI EEKARTKGEY
IKIGEI YGFSI MUKTENSSKELFDCSSNR FFVKGQBSI YYTANGKLASDPKLACQNF
INALER I PKVI ESHEKEKEKVSANKEVYMT I AGGSWKKEDELRSLKGQAAELDRKI AL
                                                                                                                                                     NKITLSYQELCEVLMREMEIKDRTAKKYIAYMKEQRILAQDSNGNYQKGELCHT'
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CDS

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INKDNLPELQRILSCIEEIMKSLNSDDYKEISEELKTEIEKDSPSRNIIKRGLQAING
IASGIVSGVIANQVSPLVTSAIALL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8333. .8428)
/locus_tag="PG0855"
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VDKAKVIYTPRMKVKTALKGVRMERAERVLDVPYASSIKPNENNSGGSSSSDNNGHAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8613.
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7293. .8111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="DNA-binding protein, histone-like family"
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9963. .10298
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                                                                                                                                                                                                                                                                                                                                            /locus_tag="PG0856"
/note="identified by
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3613. .9518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MIFSLHHFALICSEMGTFAVSKRAKYKWEVL"/
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    GB:D90325,
GB:D90330,
                                                                                                                        REFERENCE
AUTHORS
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KEYWORDS
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Query Match:
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                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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Sg

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gene

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41026 GAATTGCTAGCTCGGCGGATGCAAGTGGCATACGAGATAGGTTTGTTCAAAAAAAGAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41146 GCAGCCCTCTTAGGTTTTGGACGAAACATTTATATATCGGAGCTGTTCAGCCGTATTCATGAG 41205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41086 AATCTGGCTGGTTCAGAATCTCCGCTACGAACAACTACAGCGCAACCGTGCCCGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 GlyValProMetMetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyr 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AspThrValArgArgArgIleAspLeuGlyValArgIleAlaArgTyrLysSerArgHis
Bult, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D., Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayton, R.A., Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb. J.-F., Adams, M.D., Reich, C.I., Overbeek, R., Kirkness, E.F., Weinstock, K.G. Merrick, J.M., Glodek, A., Scott, J.D., Geoghagen, N.S., Weidman, J.F., Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kelley, J.M., Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A.,
                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 10632)
Bull, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D.,
Bult, C.J., White, O., PitzGerald, L.M., Clayron, R.A.,
Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayron, R.A.,
Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adams, M.D.,
Reich, C.I., Overbeek, R., Kirkness, E.F., Weinstcock, K.G.,
Merrick, J.M., Glodek, A., Scott, J.D., Geoghagen, N.S., Weidman, J.F.,
Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kelley, J.M.,
Feterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A.,
Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M.,
Smith, H.O., Woese, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                        Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii Science 273 (5278), 1058-1073 (1996) 96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanocaldococcus jannaschii DSM 2661
Methanocaldococcus jannaschii DSM 2661
Archaea; Euryarchaeota; Methanococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome.
U67480 L77117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GluGlnAsnGluLeuGlnArgLeuArgAlaGluLeuAspAlaLeuAspGlyThrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanocaldococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAlaAspHisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIleIleThr
                                                                                                                                                                                                 (bases 1 to 10632)
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GB:M29135, GB:M60718, GB:M73233, SP:D14101, PID
PID:184032, PID:184034, PID:213700, PID:306846,
PID:32084, and PID:337936; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:2826265
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jannaschii DSM
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Matches:
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2661
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gene	complement (16271926)	gene
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gene	₩.	gene
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	KEANPILSOVSEITHDAKTTVLSCHDEITLIJIGKSVIVTEEALEISVEADHVAKTVOKETVEMVIV TPYYNKPTQEGLRKHFGKVAES INLFIULYNVPSRTAVNLEPKTVKLLAEEYSNISAV KEANPILSOVSEITHDAKTTVLSCHDEITLIJIGKSVIVTEEALEISVEKTVANIVPKETVEMVIV	
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	` P	
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CDS	complement (59127)	gene
gene	/db xref="taxon:243232"	
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	110632	source
	te version x	COMMENT
	ısti	JOURNAL
	Venter, J.C.	TTT.8
	Kaine, B.B.,	

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putative"
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228. .2971
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WPCOMMENT
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AR271569_:
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Best Local Similarity:
Query Match:
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Fragment Nan
AR271569 00
AR271569 01
AR271569 02
AR271569 03
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AR271569 06
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                                                                                                                                                                                                                                                                                                                                                Ile
                                                                                                                                                                                                                                Name
                                                                                                                                                                                                                                                                                                                                                                                                   ArgTyrAlaAlaAspHisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIle
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/product="conserved hypothetical
/product="td="AAB98239.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="menlekklellkklreflllnlelkklmqelnvdsdlyeayekv
TKlvrepnlklyrqyydalkemfyeeygkkrkdlswypkldynrckncekclsfcprg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ferredoxin II"
/protein_id="AAB98238.1"
/db_xref="GI:1499030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="MJ0252"
/note="similar to SP:P42405 PID:710637 PID:1805418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYDAENGKVVVKYPYSCIVNCNACSIMCCENNAIIFPDEKIPRRN"
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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nuation (13
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                                                                                                                                                                                                                                                                                                                                                                      Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H., Dubois Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R., Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothier, B., Qiu, D., Spadafora, R., Vicaire, R., Wang, Y., Wierzbowski, J., Gibson, R., Jiwani, N., Caruso, A., Bush, D. and Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanothermobacter thermautotrophicus str. Delta H
(Methanobacterium thermoautotrophicus str. deltaH)
Methanothermobacter thermautotrophicus str. Delta H
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                        Submitted (10-AUG-1997) Genomics and
                                                                                                                                                                                                                                            Smith, D.R
                                                                                                                                                                                                                                                                                                                  Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics
J. Bacteriol. 179 (22), 7135-7155 (1997)
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                                                                                                                                                                     02154-8448,
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of 17) of AR271569 from base 1200001 (AR271569 Sequence 1 from patent L
                                                                                              Delta H"
                                                                                                                                 1. .13242
                   /clone="MTH"
                                    /strain="Delta H"
/db_xref="taxon:187420"
                                                                           /mol
                                                                                                                                                location/Qualifiers
note="synonym: Methanobacterium
                                                                                                             organism="Methanothermobacter"
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Street, Waltham, MA
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complement (680. .1216)

/gene="MYH797"

/note="Bunction Code:14.00 - Unknown,

/note="Bunction AC:S33068, p()=0.055, p
                                                                                                                                                                                                                                                                                                                                                                                           /note="Function Code:5.01 - L-Amino Acid Metabolism, Alanine--aspartate and glutamate metabolism; similar to, sp:LN:DHAS_METJA AC:Q57658, p()=2.4E-96, pid=55%" /codon start=1 /renduct="aspartate-semialdehyde dehydrogenase" /product="aspartate-semialdehyde dehydrogenase" /protein_id="AAB85299.1" /protein_id="AAB85299.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved protein"
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/protein id="AAB85296.1"
/db_xref="GI:2621886"
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GYFRDYPGIKRRLAEELVEHEVLGVCVDGPSVDRPGETDIHKLLLKNGIWIVENITNT
DLLPPKFRLFVVPLSVRAEASPARVFAVTGSGSGSSKDRSSFQR"
/note="Function Code:5.07 - L-Amino Acid Metabolism,
Lysine biosynthesis ; similar to, pir:LN:F64352 AC:F64352,
p()=85-80, pid=56%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown"
/product="unknown"
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/db_xref="Gi:2621887"
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/translation="MERDTMRFMRDSEKDRVIGELKGIIADKESRITDLKRYREYFQA
LTQKPEKDLTSEGQGQIYKTLPDERATTEEMLDFINEIGFKDLKLENMVQILRNLERKG
YFRSVSEGRRTLMEKVKR"
                                                                                                                                                                                                                                                          DAYTIKRVYVSTMQAVSGAGYNGVPSMAILDNLVPFIGGEEEKIETETLHLLGELDEG
VVKPASFGVSASCHRVPVVDGHTEAVFIELDDEFDIDDVREAMDKFRGLPQKLGLHSA
                                                                                                                                                                                                                                                                                                            /translation="mvnvgvlgatgmvgqrfiqmldkhpefelttlaassrsagkpyg
EVANWYLDCEMPESVRDMEVVETDPSAVGDVDILFSALPADVARKVEPKFAEKYIVAS
NASAMRMEPDVPLVIPEVNPEFLDLIEVQQRRRGWDGFIVTNPNCSTIALTLTLKFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1998. .3041)
/gene="MTH799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MHPTLLGPDLSVLYFFNSVLASPFLDFLMPLLTFGGTQAFWVIL
CLLLYLLGGEDEREAAFMALTALVLGFFLSEALKMVIARPRPYEVIGWVRHATVAGGY
SMPSGHAVAAFAGFISLYFRLGRPWFFIILASLVGISRIYLGLHYPSDVLAGAVLGVL
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/transT_table=11
/product="bacitracin transport permease related
/protein_id="AAB85298.1"
/db_xref="GI:2621888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Function Code:12.09 - Cell Processes, Protein
peptide secretion; similar to, sp:LN:Y374_METJA
AC:Q57819, p()=1.7E-13, pid=28%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MTH798"
complement(1431. .1991)
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/gene="MTH797"
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/note="Function Code:14.01 - Unknown, Conserved protein;
similar to, pir:LN:G64397 AC:G64397, p()=5.5E-17, pid=30
                                                                                                                 complement (3054. .3875)
                                                                                                                                                                                                      ASILNAELINEIL"
                                                                                                                                                                                                                                PEKPVVVRDEENRPQPRMDRDMDGGMAVTVGRLREDAAFKNSLRYVLVGHNTVRGAAG
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62. .676
                                                                                       /gene="MTH800"
                                                                                                                                              /gene="MTH800"
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/transl_table=
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Ribosomal proteins; similar to, sp:LN:R17E_METJA
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complement (4776. .5996)
/gene="MTH802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGESATITHEEQRRMIDILVDEVNGRVRTVAGAGSNSSREAMGLVEYAEDAGADAAL
VITPYYNKPOPHGLIEHYTMLEEAADIPLIIYNVESRTGTDIDVDTVABLAKLDGIIG
IKBASPDLDKVSMLRSRLMDLGLDDFTVLSGNDNLTLPMISMGAEGVISVVANVDPAR
MSRLVNEALSGDFESAMKTHYELYSLMKVLFIESNPVPVKEALNMMGKARGSCEDAPG
TPAGCKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSLSLGRDIAMITISSPDFIDTPGIISEITKPLRDNDLNIVEISSSQTSVVIFVDWN
DGKKAYELVRGVLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MELIVAKFGĞTSIGNGRRIKKAARSVVKEYMKGRKVVVVVSAIN
KTTDELLQIVDEAMEDAVTEKQLÄE IVSMGENTSVRIFSSAIEALGVKSEYIDFFMDE
WPIITDSNLLAKKUPEATEEKSRELLKLLDGOIIFVVGGFLGRDPNGYITTLLGRGS
DITAFLLGHCLKADEVIIVTDVGĞVMSTDPNKLQGAKKLDKISVEEMRDLATHGAQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/db_xref="GI:5021891"
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IGEFTGRGSVGVEVTDASNLADTLAETEPDVLVDFTVASAAVETIKTSTEAGVNLVVG
TTGFSEEEMQTVRDCIERSGVRAVIAPNMAVGVNVPFKVLRDLAPILSDYDVEIIEAH
                                                                                                                                                                                                                                           complement (6236. .6532)
                                                                                                                                                                                                                                                                    complement (6236.
/gene="MTH804"
                                                                                                                                                                                                                                                                                                                          /trānslation="MGNIRTSFVKRIAKEMIETHPGKFTDDFDTNKKLVEEFSTVSTK
HLRNKIAGYITRIISQQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPHALKYKDPDIKAKI IGFEHGDLSAPGTE I IGPSKNKMYKTTTLNPDP I SVVAVVGE
KILNKPGILARLTSRLAENS I NI IGISTGQNSVT I FVDKKDADEAHRLLHDVV I ADDD
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Lysine biosynthesis ; similar to, sp:LN:DAPA_METJA
AC:Q57695, p()=1.5E-69, pid=50%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3928. .4779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDHIVLFAGDGERLEIVHRAHSRDAFIGGVIRAIRFIEDAEDGRIMDMGDVLGIN"
complement (3928. .4779)
                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB85303.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MTH803"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4776. .5996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MKIEGTVVAMVTPFTEDDVVDEAGLRENINYLIENGVDGLLVAG/
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                                                                                                                                                                                                                                                                                                                                                                                                                                   product="ribosomal
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                                                                                                                                                                                                                                                                                                .6532)
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                                                                                                                                                                                                                                                                                                                                                                                                                  protein S17°
)3.1°
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                                                                                                                                                pid=32%"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: October Job time: 1687.4 secs
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                                                                                                          6325
                                                                                                                                                               6385
                                                                                                                                                                                                                                                                        6505
                                                     6268 ACTGAACAGAAAGAAATGTTAAGG
                                                                                                                                                                                                                  6445 TCAAGGATAGCCCTTGCACGGGAGATAGCAGAGGCCCAAGGAGGTCCTTGGAATGGAGATC 6386
                                                                                                                                     67
                                                                                                                                                                                   47 MetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyrAlaAlaAspHis 66
                                                                               87
                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                     7 LeuGlnArgLeuArgAlaGluLeuAspAlaLeuAspGlyThrLeuLeuAspThrValArg
                                                                                                       ArgArgIleAspLeuGlyValArgIleAlaArgTyrLysSerArgHisGlyValProMet 46
                                                                             ValGluAspLeuValMetSerArg
                                                                                                                                                             CTGGATCCTGAAAGGGAACTCCAGATTATAGAGAGGACCCGGAAAATCGCCAGGGAAAAT
                                                                                                                                                                                                                                                                       CTCAGAAGATCCAGGCAGAAGATAGATGGAATAGACAGGGACATACTTGACCTCATAACC 6446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGMEILDPERELQIIERTRKIARENGIDENKLTELMKILMDLSKTEQKEMLRRQ"
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similar to, pir:LN:G64479 AC:G64479, p()=1.8E-36, pid=31%"
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            2005, 15:30:35
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                               94
                                                     6245
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26
22
22
39
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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool h/US10089514/runat_04102005_105743_8027/app_query.fasta_1.1621
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-DB=N_Geneseq -QEMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=+5
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10089514 @CGN_1 1 860 @runat_04102005_105743_8027 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NORM=ext -HEAPSIZES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          514
514
486.5
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256
                                                                                                                                                             Score
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seq length: 2000000000
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Ygapop 10.0 , X
Fgapop 6.0 , F
Delop 6.0 , I
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Aaf86410 4-amino-4
AalS0181 S venezue
Abz69799 Plasmid p
Abz69798 Plasmid p
Aat58552 Streptomy
                                                                                                                                                        Description
     RESULT 1
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ALIGNMENTS

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Streptomyces venezuelae
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                                          29-SEP-1999;
                                                                                     29-SEP-2000; 2000WO-JP006783
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Murakami
28-JAN-2003
                              AAL50181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transformant producing secondary metabolite modified with functional group e.g. benzene with nitrogen-containing substituent at para-position, PF1022, with ease at low cost, for application in pharmaceuticals and
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                                                                                                                                                                                                                                                                                                                                               The present invention relates to transformants capable of producing PF1022 substance derivatives. These were obtained by transferring a gen participating in the biosynthesis pathway from chorismic acid to paminophenylpyruvic acid (biosynthesis gene) into a phenylalanine-requiring host derived from an organism producing the PF1022 substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel biosynthesis gene-transferred tr. substance derivatives by fermentation, drugs with anthelmintic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 85; 116pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2001; 2001JP-00082227
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ine; p-aminophenylpyruvic acid; pharmaceutical;
drug; gene; ds.
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                                                                                                                                   The invention relates to a novel composition comprising a translation comprising an orthogonal tRNA (O-RNA) and an orthogonal aminoacyl CENA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-ERNA with at least one unnatural amino acid in the translation system and the O-ERNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the AsplITMG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse collydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse collydrofolate reductase comprising CHOOH Hisfeag. The unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid containing the individual genes papABC that encode the enzymes used to carry out the conversion of chorismate to the unnatural amino acid p-aminophenylalanine (pAF)
                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                aminoacyl tRNA synthetase.
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Pastrnak M,
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The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacy tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the -tRNA with at least one unnatural amino acid in the translation system and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Aspl2TAG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse
                                                                                                                                                                                                                           Schultz
Meggers
                                                                                                                                              Composition useful for producing has translation system comprising aminoacyl tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHFR; translation; orthogonal tRNA; O-tRNA; O-RS; CAT; Tyrk: orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase;
                                                                                                                                                                                                    WPI; 2003-120430/11.
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06-FEB-2002; 2002US-0355514P
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                       Example 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis;
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                                                                                                                      Page 124-127; 188pp; English.
                                                                                                                                                                                                                            Wang 1
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RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptogramin B; antibiotic; biosynthesis; pristinamycin; virginiamycin; DMPAPA precursor; 4-dimethylamino-L-phenylalanine; papA; papM; papB; papC; isomerisation; aromatisation; N-methyltransferase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces
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                                                                                                                                                                                                                                                                                                                        mat_peptide
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(pAF) in vivo
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                                                       94FR-00008478.
                                                                                                      95WO-FR000889
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                                                                                                                                                                                                                                                                      /product= "PapB"
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Best Local S Query Match:

Similarity:

1.03e-25 256.00 71.08% 61.45% 49.81%

Gaps:

Mismatches: Indels:

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Length:
Matches:
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Score:

Alignment Scores:

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The papA and papM genes of S.pristinaespiralis are involved in the biosynthesis of 4-dimethylamino-L-phenylalamine (DMPAPA), a precursor for pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papC) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The papC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DMPAPA synthesis. The second open reading frame
                                     (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is likely to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-deoxy 4-aminoprephenate acid. Disruption of the papB and papC genes can be used to produce strains of S.pristinaespiralis which are unable to produce the antibiotic pristinamycin I but which may be able to produce new, modified forms of it
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e L, Famechon
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Paris J, Dutruc-Rosset
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Streptogramin B; antibiotic; biosynthesis; pristinamycin; virginiamycin;

pristinaespiralis papA and papM intergenic region

Streptomyces

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                    Alignment Scores:
                                                                                                                                                                         complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The PapC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DWPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is likely to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-
                                                                                                                          deoxy 4-aminoprephenate. Disruption of the paph and papC genes can used to produce strains of S.pristinaespiralis which are unable to produce the antiblotic pristinamycin I but which may be able to pronew, modified forms of it
                                                                                                                                                                                                                                                                         The papA and papM genes of S. pristinaespiralis are involved in the biosynthesis of 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papC) was on the
                                                                                                                                                                                                                                                                                                                                                                             New streptogramin B derivs. useful as antibiotics - produced by mutants of Streptomyces having altered genes for streptogramin
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e L, Famechon
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US-10-089-514-4 (1-103)

x AAT59268 (1-2888)

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RESULT 7
ACF71772
The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antiblotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; fungicide; insecticide; polymorphism; genetic and detection; food; gene expression; plant; animal; microorganism; antibiotic; biopesticide; virulence factor; disease model; plagn
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US-10-089-514-4 (1-103) x ADM27081_16
Bacterial polynucleotide #1138
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                                                                                            standard; DNA; 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1125 BP; 352 A; 180 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new Proteus mirabilis polypeptides and polynuclectides. The invention also relates to antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1138; 870pp; English
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                                                                      ArgValGluAspLeuVal-----MetSerArgGluSerLeuThrAlaGluAsp 101
                                                                                                            ATGGGTATTTCTGCTGATTTA--
                                                                                                                                                                                  ATCTATGCACCAGATAGAGAAGCCGCAATGCTTGCTTCTCGACGTAATGAAGCAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1305
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Klebsiella J
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                                                                    ACTATCGGCAAGCGCCATAATCTGGATGCGCACTATATCACCCGCCTGTTCCAGCTGATT
                                                                                                        ArgTyrAlaAlaAspHisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIle
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RESULT 14
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Best Local Similarity:
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Pred. No.:
                                                                                                                      27-OCT-2003
02-APR-2003
                                                                                                                                                                                                        invention are useful for producing a plant such as canola, maize, Arabidopsis, Brassica campestris, B.napus, soybean, crambe, mustard, castor bean, peanut, sesame, cottonseed, linseed, safflower, oil palm, flax and sunflower having increased tocopherol levels, especially alpha-or gamma-tocopherol or tocotrienol relative to a plant with a similar genetic background but lacking the exogenous nucleic acid molecule. They are useful for reducing tocopherol levels in a plant. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthesis useful for enhancing or al plants such as canola, maize, soybean, peanut, sesame, or cottonseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule encoding enzymes involved in tocopherol biosynthesis useful for enhancing or altering tocopherol production plants such as canola, maize, soybean, crambe, mustard, castor bean,
                                                                                                                                                                              useful for producing plant expressing homogentesic acid and plastoquinones. The present sequence is Erwinia herbicola bifunctional
                                                                                                                                                                                                                                                                                                               chorismate mutase activities or a tyrA from Erwinia herbicola or Escherichia coli bifunctional prephenate dehydrogenase. Sequence
                                                                                                                                                                                                                                                                                                                                             production of an mRNA molecule linked to a heterologous nucleic acid molecule encoding an enzyme with prephenate dehydrogenase (tyrA) or
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel nucleic acid molecules encoding enzymes involved in tocopherol biosynthesis. Polynucleotides of the invention comprise a promoter region functioning in a plant cell to ca
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                                                                                                                      Sequence 1122
                                                                                                                                                                prephenate dehydrogenase DNA.
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                                                                                                                                                                       The invention relates to a novel substantially purified nucleic action molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought resistant biosynthesis and in producing plants with increased drought biosynthesis and in producing plants with increased drought biosynthesis and in producing plants with increased drought biosynthesis and in producing plants with the plants with the plants with the plants with the plants with the plants with the plants with the plants with the plants with the plants with the p
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05-AUG-2003; 2003US-00634548.
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-DB=Issued Patenits NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-DB=Issued Patenits NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE.pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=sex -HEARSIZE=500 -MINLENS=0 -MAXLEN=2000000000
-USER=US10089514 @CGN 1 1.116 @runat 04102005 105746_8071 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DS9BLOCK=100 -LONGLOG
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-765-907A-4
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8770,	Sequence 1471, Ap	682,	7256,	19, 7	1	19,	Sequence 1090, Ap	æ	Sequence 19, Appl	Sequence 1, Appli	Sequence 9326, Ap	Sequence 785, App		U	5778,	10473,	w	e 10259,	5815,	25	e 159		18	1320,	e 1, 2	e 1, 7	4684,	4724,	e 4705,	9 4814,	e 126	5637,

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: THIBAUT, Denis
APPLICANT: HAMAS-JACQUES, Nathalie
APPLICANT: BLANCHE, Francis
APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: PAMECHON, Alain
APPLICANT: PAMECHON, Alain
APPLICANT: DPAIS, Jean-Marc
APPLICANT: DTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                             US-08-765-907A-4
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                                                                                                                                                                                                                 SEQ ID NO 4
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. :
                                                                                                                                                    TYPE: DNA ORGANISM: Streptomyces pristinaespiralis
                                                                                                                                                                                               LENGTH: 387
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 4.96e-28
256.00
71.08%
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Matches:
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US-09-987-614A-4
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CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Streptogramins And Method For Preparing Same
TITLE OF INVENTION: Mutasynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BLANC, Veronique APPLICANT: THIBAUT, Denis
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                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 387
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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                                                                124 ACACGCCTGGACATCTGCCTGCGCATCGGCGAGTACAAGCGCCCTCCACCAGGTGCCGATG
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                   MetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyrAlaAlaAspHis
                                                                                                                                   CTCGACGCGCTGCGCCCGCCTGGACGCCGGGACGCCCTGCTGGACGCCGTCCGC
                                                                                         ArgArgIleAspLeuGlyValArgIleAlaArgTyrLysSerArgHisGlyValProMet
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DUTRUC-ROSSET, Gilles
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DEBUSSCHE, Laurent
FAMECHON, Alain
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BAMAS-JACQUES,
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Matches:
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Indels:
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RESULT 4
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Best Local Similarity:
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US-08-765-907A-1
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Sequence 1, Application US/09987614A Patent No. 6833382 GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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APPLICANT: THIBAU
APPLICANT: BAMAS-
APPLICANT: BLANCH
APPLICANT: COUZET
APPLICANT: BARRIE
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CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same
TITLE OF INVENTION: Mutasynthesis
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DUTRUC-ROSSET, Gilles
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COUZET, Joel
BARRIERE, Jean-Claude
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FAMECHON, Alain
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BAMAS-JACQUES, Nathalie
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Conservative:
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APPLICANT: BLANC,

Veronique

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Sequence 1, Application US/08916421B
Patent NO. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Se
Patent No. 6503729
Patent No. 6503729
TITLE OF INVENTION: jannaschii
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SEQ ID NO 1
                             SEQ ID NO
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                                             CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin version 3.1
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CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                FILE REFERENCE: PB275
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TYPE: DNA
             LENGTH: 1664976
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DUTRUC-ROSSET, Gilles
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BAMAS-JACQUES, Nathalie
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LOCATION: (234814). (234814)
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                                                                    LOCATION: (309398) .. (309398)
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LOCATION: (309418) .. (309418)
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LOCATION: (312837) ... (312837)
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LOCATION: (234187)...(234187)
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LOCATION: (148948)...(148948)
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LOCATION: (98266)..(98266)
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NAME/KEY: misc feature LOCATION: (1569020)..(1569020) .. OTHER INFORMATION: n equals a,
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LOCATION: (1119881)...(1119881)
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LOCATION: (1470091)..(1470091)
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LOCATION: (855539)..(855539)
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LOCATION: (779455)...(779455)
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LOCATION: (600992)..(600992)
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LOCATION: (559241)...(559241)
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                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Complete Genome Patent No. 6797466
TITLE OF INVENTION: jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09692570 Patent No. 6797466 GENERAL INFORMATION:
                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/692,570 CURRENT FILING DATE: 2003-01-14 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 PRIOR APPLICATION NUMBER: US 08/916,421 PRIOR APPLICATION NUMBER: US 08/916,421 PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PB275C1
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                                                    NAME/KEY: misc feature
LOCATION: (28222) ...(28222)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
                                                                                                           ORGANISM: Methanococcus FEATURE:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (234220)...(234220)
OTHER_INFORMATION: n equals FEATURE:
NAME/KEY: misc_feature
LOCATION: (98239)...(98239)
OTHER_INFORMATION: n equals FEATURE: NAME/KEY: misc_feature
LOCATION: (84773)...(84773)
OTHER_INFORMATION: n equals NAME/KEY: misc feature LOCATION: (309398)...(309398) OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
FEATURE: FEATURE:

NAME/KEY: misc_feature
LOCATION: (234187) ... (234187)
CTHER INFORMATION: n equals FEATURE:

NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (191995)..(191995) OTHER_INFORMATION: n equals NAME/KEY: misc feature LOCATION: (163385)..(163385) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc feature LOCATION: (148948)...(148948) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc_feature LOCATION: (103998)..(103998) OTHER INFORMATION: n equals FEATURE:
NAME/KEY: misc_feature
LOCATION: (98256) ... (98266)
OTHER_INFORMATION: n equals FEATURE:
NAME/KEY: misc_feature
LOCATION: (98159)...(98159)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (98120)..(98120) OTHER INFORMATION: n equals FEATURE:
NAME/KEY: misc_feature
LOCATION: (84808)...(84808)
OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (191989)...(191989) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc_feature LOCATION: (98343)..(98343) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (84812)...(84812) OTHER INFORMATION: n equals FEATURE: OTHER INFORMATION: n equals a, a, a a u ø 9 çı a, a a a e G a, a a, a, à a , ŗ ,, ŗ ŗ ŗ , , , ŗ ŗ ŗ ζ, ۲ ņ ú ç ņ ç ç ņ ņ ó ç ú ç ů ú ũ ņ ņ ņ ņ ဓ္ or 9 õ or P or or õ or õ õ ဝူ Ö, õ 8 g or or or ω g g ω ω ω g Ω ø g ω g ω ω ω ıΩ ω

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Sequence 1138 Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITILE OF INVENTION: NUCLEIC ACID AND THERAPEU FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR TILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1138
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Query Match
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
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LENGTH: 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4503, Application Patent No. 6610836
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Klebsiella
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ORGANISM: Proteus
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                 CTGCTTGCTCTGCTGGCGGAGCGCCGCGGACTGGCTGGAGGTTGGAAAAGCCCAAACTG
                                          LeuLeuAspThrValArgArgIleAspLeuGlyValArgIleAlaArgTyrLysSer
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US-10-089-514-4 (1-103) x US-09-489-039A-4503 (1-1305)
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APPLICANT: Gary Breton et. al
APPLICANT: USENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION UNMERS: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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ATGACCGAGGAAAACCCATTACTGGCGCTGCGCGATAAGATAAGCGCCCTGGACGAAG
                                        MetThrGluGlnAsnGluLeuGlnArgLeuArgAlaGluLeuAspAlaLeuAspGlyThr
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Stater, Steven C.
FITLE OF INVENTION: Myxococcus xanthus Genome Secons Reference: 38-10(15049)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
FRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2740
LENGTH: 1963
TYPE: DNA
COCANICAN MAYOCOCCUS Xanthus
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US-09-902-540-2740
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                 Sequence 1129, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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Patent No. 6833447
     APPLICANT:
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Goldman, Barry S.
Hinkle, Gregory J.
Slater, Steven C.
Wiegand, Roger C.
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Best Local Similarity:
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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FILING DATE: 31-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                         STREET: /52 CITY: Palo Alto
                                                                                                                      FILING DATE: 2: CLASSIFICATION:
                                                                                                                                                           APPLICATION NUMBER:
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    JMBER: PP1546
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                                                                                                                                                                                                  Version
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PRIOR APPLICATION DATA:

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Query Match:
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SEQ ID NO 4572
LENGTH: 1131
TYPE: DNA
                                                                                                                                                                                          Sequence 4572, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                            APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEG ID NOS: 14342
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LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: PCT/AU98/01023
FILLING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
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Conservative:
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Gaps:
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US-09-902-540-5637
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DB:
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Best Local Similarity:
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US-09-489-039A-4572
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5637
LENGTH: 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Myxococcus
                                                                                                                                                                                                                                                                   No.:
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                                                                      775 CTGACGGAAGTTCGGGAGTGCGTGGATGCGTTGGACCTGGTTCAACTCCTGAAT
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                         ArgArgIleAspLeuGlyValArgIleAlaArgTyrLysSerArgHisGlyValProMet
                                                                                          LeuGlnArgLeuArgAlaGluLeuAspAlaLeuAspGlyThrLeuLeuAspThrValArg
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Serile Reference: 38-10(15849)B
CURRENT APPLICATION UMMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1269
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US-09-252-991A-4814/c
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US-09-902-540-1269/c
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                                                                                                                                                                                                                                                                         Sequence 4814, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AUGUSIOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4814
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TYPE: DNA
ORGANISM: Myxococcus xanthus
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Best Local Similarity:
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                                                                                66 HisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIleIle
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-QG/Cgn2 1/USPTO_spool h/US10089514/runat_04102005_105745_8055/app_query.fasta_1.1621
-DB=Published_Applications_NA -QRMT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNTS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10089514 @CGN 1 1 920 @runat_04102005_105745_8055
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Fgapop 6.0 , E
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. NO. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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87-3 3, Application U on No. US2004021 NFORMATION: T: YANAI, KOji T: SUMIDA, Naomi T: WATANABE, Ma T: WATANABE, Ma T: MURIYA, Tats T: MURAKAMI, Tats T: MURAKAMI, Tats T: MURAKAMI, Tats T: MURAKAMI, Tats T: MURAKTION: Tran INVENTION: Tran INVENTION: 2003-130 APPLICATION NUMBER FILING DATE: 20				14.2				14.2			14.6	14.6	14.6						•	•			•	17.2		٦.		17.5	٦,			19.8		19.8		- ;	Query Match
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37 3 Producing Substance Same And Novel 11144 1)472,587	ALIGNMENTS	S-10-156-761-	US-10-320	US-10-320	US-10-461	US-10-440	US-10-440	US-10-241	US-10-156	US-10-369	US-10-47	US-10-102	US-10-027	US-10-027-632-16649	US-10-472	US-10-767	US-10-027	US-10-027	US-10-027	US-10-027	US-10-027	US-10-335	US-10-156	US-10-98	US-10-15	US-10-282-122A	US-10-380-132-7	US-10-433-556-	US-10-156-761-	US-10-156-761-6	US-10-381-779-4	US-10-433-556-20	US-10-634-548-1	US-10-137-310-1	US-10-126-927-	IIS-10-472-587-	ID
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 312
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             APPLICANT: Pastrnak, Miro
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                   APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Mang, Lei
SOFTWARE: PatentIn version 3.1
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ORGANISM: Streptomyces
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LOCATION: (1)..(309)
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Liu, David R
Magliery, Thomas
Meggers, Eric L
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; ORGANISM: Plasmid pSC101, Streptomycese venezuelae papABC
US-10-126-927-67
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; ORGANISM: Streptomyces venezuelae
US-10-126-927-68
                                                                                                      APPLICANT: PASETNAK, MIRO
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
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                            NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 12391
TYPE: DNA
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Publication No.
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APPLICANT:
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APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Wang, John C
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No. US20030082575A1
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Meggers, Eric L
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Liu, David R
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Sequence 1, Application US/10137310
Publication No. US20030176675A1
GENERAL INFORMATION:
APPLICANT: Valentin, Henry E.
APPLICANT: Miesky, Timothy A.
TITLE OF INVENTION: TyrA Genes and Uses Thereof
FILE REFERENCE: 16515.147
CURRENT APPLICATION NUMBER: US/10/137,310
CURRENT APPLICATION NUMBER: US/00/289,527
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 12
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Best Local Similarity:
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SEQ ID NO 1
LENGTH: 1122
TYPE: DNA
ORGANISM: Erwinia herbicola
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GAACTGACCGCGTTACGCGATCAAATTGACAGTGTAGATAAAGCGCTGCTGGATCTGCTG
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US-10-634-548-16
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; TYPE: DNA
; ORGANISM: Erwinia
US-10-634-548-16
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APPLICANT: Woshiri, Farhad
APPLICANT: Stein, Joshua C.
APPLICANT: Valentin, Henry E.
APPLICANT: Venkatesh, Tyamagondlu V.
APPLICANT: Venkatesh, Tyamagondlu V.
APPLICANT: Venkatesh, Tyamagondlu V.
CILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: us 60/400,689
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
COUNTAINE DEFERTING USFAIR 12
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                                      211 ---ATTGAGGATGTGCTGCGTCGCGTGATGCGGGAATCCTATACCAGCGAGAAT 261
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                                                                                                                                                     66 HisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIleIleThrGluMetCys
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                                                               ArgValGluAspLeuVal-----MetSerArgGluSerLeuThrAlaGluAsp 101
                                                                                                                    CTCGGCGTACCACCGGATCTG---
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                                                                                                                                                                                                                                                                     GAACTGACCGCGTTACGCGATCAAATTGACAGTGTAGATAAAGCGCTGCTGGATCTGCTG
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Hirshberg, Joseph
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Matches:
Conservative:
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Indels:
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US-10-194-163-361/c
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1 US-10-433-556-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
                                                                                                                                                                                                                                                                                Sequence 361, Application US/10194163 Publication No. US20020172976A1 GENERAL INFORMATION:
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Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 5500*120
CURRENT APPLICATION NUMBER: US/10/433,556
CURRENT FILING DATE: 2003-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matringe, Michel
APPLICANT: Rippert, Pascal
TITLE OF INVENTION: Novel Targets For
TITLE OF INVENTION: Said Herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Erwinia herbicola FEATURE:
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ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                               APPLICANT: Ross, Bruce Carter
                                                                                                                                                                                                                                                                                                                                                                                   211 ---ATTGAGGATGTGCTGCGTCGCGTGATGCGGGAATCCTATACCAGCGAGAAT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 CTCGGCGTACCACCGGATCTG-
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                                                                                                         COUNTRY: USA
                                                                                                                             STATE:
                                                                                                                                            CITY: PALO ALTO
                                                                                                                                                                STREET:
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50.00%
27.55%
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Indels:
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Conservative:
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US-10-381-779-40/c
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CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-089-514-4 (1-103) x US-10-194-163-361 (1-850)
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                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10381779 Publication No. US20030219798A1 GENERAL INFORMATION:
                                                                                                                                                                                  APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
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INFORMATION FOR SEQ ID NO: 361
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 GAATTGCTAGCTCGGCGGATGCAAGTGGCATACGAGATAGGTTTGTTCAAAAAAGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GlyValProMetMetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyr
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION: <Unknown>
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LOCATION: 1...850
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Matches:
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Sequence 6187, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6187
LENGTH: 387
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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Best Local Similarity:
Query Match:
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; ORGANISM: Sphingomonas
US-10-381-779-40
                                                                                Pred.
                                                                                                   Alignment Scores:
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LENGTH: 1833
                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                ORGANISM: Streptomyces avermitilis FEATURE:
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17.70%
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                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLB OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: DATE: 201-08-02
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SEQ ID NO 1
LENGTH: 9025608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (4187715)
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                                       7459306 GCCGAACGCTTCAAGTGCACCCAGCAGGTCGGCCACCTCAAAGCCGTACACCAGCTGCCG 7459365
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46 MetMetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyrAlaAlaAsp
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Sequence 3, Application US/10137310

Publication No. US20030176675A1

GENERAL INFORMATION:

APPLICANT: Valentin, Henry E.

APPLICANT: Witsky, Timothy A.

TITLE OF INVENTION: TyrA Genes and Uses Thereof

FILE REFERENCE: 16515.147

CURRENT APPLICATION NUMBER: US/10/137,310

CURRENT FILING DATE: 2002-05-03

PRIOR APPLICATION NUMBER: US 60/289,527

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0

SEQ ID NO

SEQ ID NO

TYPE: DNA

OPGANISM. Escherichia Coli
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Query Match:
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US-10-137-310-3
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                                                                                                                Sequence 18, Application US/10433556 Publication No. US20040117872A1 GENERAL INFORMATION:
   APPLICANT: Matringe, Michel
APPLICANT: Rippert, Pascal
TITLE OF INVENTION: Novel Targets For
TITLE OF INVENTION: Said Herbicides
FILE REFERENCE: 5500*120
CURRENT APPLICATION NUMBER: US/10/433.
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   APPLICATION NUMBER: US/10/433,556
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                                                                                                                                                                                                                                                        CysArgValGluAspLeuVal-----MetSerArgGluSerLeuThrAlaGluAsp 101
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.
SEQ ID NO 18
LENGTH: 1122
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
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Best Local Similarity:
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                                                                                                            FEATURE:
NAME/KEY: CDS
NAME/KEY: (25)..(1143)
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10380132
Publication No. US20030182679A1
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SunGene GmbH & Co. KGAA
TITLE OF INVENTION: Improved processes for vitamin
FILE REFERENCE: NAE445/2000
CURRENT APPLICATION NUMBER: US/10/380,132
CURRENT FILING DATE: 2003-03-11
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                               FEATURE:
NAME/KEY: gene
LOCATION: (7)..(1232)
OTHER INFORMATION: tyrA gene coding for bifunctional chorismate
OTHER INFORMATION: mutase / prephenate dehydrogenase
FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: (1233)..(1238)
                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(6)
                                                                                                                                                                                                                                                                                      LENGTH: 1238
TYPE: DNA
ORGANISM: Escherichia coli
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LOCATION: (1)..(1122)
                                                           OTHER INFORMATION: restriction
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                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
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                                                                                                                                                          APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06 APPLICATION NUMBER: 60/230,347
                                                                                   APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625
                                             APPLICATION NUMBER:
                                                                                                                                             FILING DATE: 2000-09-09
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               APPLICATION
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Zyskind, Judith
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             NUMBER: 60/267,636
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Remaining Prior Application data remove,
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15346
LENGTH: 1104
TYPE: DNA
ORGANISM: Clostridium acetobutylicum
US-10-282-122A-15346
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/643,990 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/329,670 CURRENT FILING DATE: 2002-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome,
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1
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                                 NAME/KEY: misc feature
LOCATION: (10150)...(10150)
OTHER INFORMATION: n equals
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                    ORGANISM: Haemophilus influenzae FEATURE:
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LOCATION: (55369)..(55369)
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
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LOCATION: (139910)...(139910)
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LOCATION: (147197)...(147197)
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LOCATION: (145942)...(145942)
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                                               1370586 TATGCGCCAGAACGTGAAATAGCAATGCTCCAAGCACGT 1370624
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1370526 AAACGTCTTGAGTTGGTTTCTCAAGTCGGTAAAGTGAAACATCAACATGGATTACCTATT 1370585
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(Uspło) Angle Blank (Uspło)

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_Bpool h/US10089514/runat_04102005_105744_8043/app_query.fasta_1.1621
-Q=/cgn2 1/USPTO_Bpool h/US10089514/runat_04102005_105744_8043/app_query.fasta_1.1621
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMAYCH=0.1 -LOOPEL-0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=USL10089514_@CGN 1_1 6050 @runat_04102005_105744_8043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

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PRI0149c F10 2 - PRI0149c.BR (806) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic CL688507

VERRION CL688507.1 GI:50197585

SOURCE CL688507.1 GI:50197585

SOURCE Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 806)

AUTHORS AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

FEATURES Location/Qualifiers

Source /organism="Pristionchus pacificus" / nol_type="genomic DNA"

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RESULT 2
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Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Unpublished (2004)
Contact: J Hopkins
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                                                                                                                                                                                                                                                             Seq primer: Ml3reverse High quality sequence :
                                                                                                                                                                                                                                                                                         Email: j.hopkins@ed.ac.uk
Plate: 02 row: E column
                                                                                                                                                                                                                                                                                                                Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN822873 TG:47950942
CN822873.1 GI:47950942
EST.
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Mammalia; Eutheria;
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02E15_M13reverse Sheep
NA clone Oa_splbn_02E15
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/db_xref="taxon:54166"
/clone lib="Mixed stage fosmid library of P.
var. California"
                                                                                                                                /clone="0a_splbn_02E15"
/clone_lib="Sheep spleen\brain pSport1 library"
/note="Vector: pSport1"
                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                     organism="Ovis aries"
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goo,Y., Roach,J., Glusman,G., Baliga,N.S., DasSarma,S., Ng,W.V. and Hood,L.
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Natrialba asiatica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NaRP11_0120 Na p
survey sequence.
                                                                                                                                                                                                                                                                                                                                        Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                      Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                                                                                                                                                                                                                 Institute for Systems Biology
1441 North 34th Street, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Goo Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacteriaceae; Natrialba.
1 (bases 1 to 600)
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(1-103)
                                                                                                                                                                                                                                                                                                                             shotgun.
                                                                                                                                                                   /clone_lib="Na pUC18 Library"
/note="Vector: pUC18; Site_1: SmaI; A shotgun library
constructed from Natrialba asiatica genomic DNA using
pUC18/SmaI/BAP plasmid"
                                                                                                                                                                                                                                /strain="ATCC 700177"
/db_xref="taxon:64602"
                                                                                                                                                                                                                                                             organism="Natrialba asiatica"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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BZ895453

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                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                     Email: black009@niehs.nih.gov
Clone is available through Rese.
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fi
cdna@resgen.com
DNA Sequencing and analyses pe.
Health Intramural Sequencing Ce.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 2770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Start, M.B. The NIEHS xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs
                                                                                                                                                                                                       Seq
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BACKWARD: CAGGAAACAGCTATGAC
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Xenopus laevis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 471)
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        /dev_stage="unfertilized egg"
/lab_host="DH108"
                                                                                                    /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="PBX0056H07"
                                               tissue_type="unfertilized egg"
cell_type="unfertilized egg"
                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                        CAGGAAACAGCTATGACC
                                                                                      'sex="female"
                                                                                                                                                                                                                         row: H column:
_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                                                                                                                         Research Genetics, Inc.,
                                                                                                                                                                                                                                                                                          performed by National Institutes of Center (NISC).
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                                                                                                                                                                                                                                                                                                                                        fax 256-536-9016 att:cdna, email
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approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT773-Pac vector. The library contained approximately 7.2 X 10⁵ recombinants, with average insert sizes of 1-1.5 kb." /note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two

2.4 79.00 50.48% 26.67% 15.37%

Length: Matches:

Gaps:

Mismatches: Indels: Conservative:

MMENT	JOURNAL	TITLE	AUTHORS	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ORCE	YWORDS	RSION	CESSION	FINITION	CUS	SULT 5 674789												
	•	dB database for the nematode satel	Srinivasan.J., Otto.G.W., Kahlow,U., Geisler,R. and Sommer,R.J.		Filkaryota: Metazoa: Nematoda: Chromadorea: Diplogagterida:	Pristionchus pacificus	GSS.	CL674789.1 GI:50178309	•	pacificus var. California Pristionchus pacificus genomic, genomic	Tinear GSS 09-JUL-20		292 CCGGATGTGGCGCAG 306	96 SerLeuThrAlaGlu 100	244 TTGAGGCAGGAGAATTGCCGGTTATCGGAACTCCTTCAGACGCAAGAG 291	76 LeuTyrAspVallleIleThrGluMetCysArgValGluAspLeuValMetSerArgGlu 95	184 CGGCAGAGGAGAGAGAGGCTGCAGAACACAGGATGTCTCTAAATGCTCTGGAAAAC 243	56 LysAspArqAlaAlaArgTyrAlaAlaAspHisGlyLeuAspGluSerPheLeuValAsn 75	130 ATCAGAATGGCTTCCAGTGCAGGCATCGACTGGGAGAGGAAAATTAAAGCCGAA 183	36 AlaArgTyrLysSerArgHisGlyValProMetMetGlnProGlyArgValSerLeuVal 55	70 GTGCTGGATGGGATGAGGAAGGAGATCTCACAGGCTCACTCA	21 LeuLeuAspThrValArgArgArgIleAspLeuGlyValArgIle 35	10 AGGTCTGAAAATAAAAAGCTGAAAGGCCAGCTCTCACAGGCTGAGCTGACCCCACAAGAGC 69	4 GlnAsnGluLeuGlnArgLeuArgAlaGluLeuAspAlaLeuAspGlyThr 20

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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
                                             Unpublished (2002)
Contact: Cordonnier-Pratt MM
Contact: Cordonnier and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-72
Tel: 706 542 1860
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                                                                                                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plant
                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
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BM326074.1 GI:18065211
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                mmpratt@uga.edu
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/clone_lib="Mixed stage fosmid library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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   have
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                                                                                                                                                                                                                                                                                                                                                                     226 GAGAACCGCCGACTCGACGCCGAGCACCGCGTCGGAGTCGATGATGTCTTTCTCAGG 167
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                                           BH454175 692 bp DNA line BOGIX86TF BOGI Brassica oleracea genomic clone
survey sequence.
BH454175
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                                                                                                                                                                       ACGGCGACCATCGACGAGAACCGCCGA
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/note="Vector: pBluescript II SK(-) from Lambda Zap II;
Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRM42I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: while most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/cultivar="BTx623"
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                                             linear GSS
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GSS.
AGENCOURT 10492829 NICHD XGC_OO1 Xenopus laevis cDNA clone IMAGE:6642739 5', mRNA sequence.
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1 (bases 1 to 692)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Franceun, C.D., Van Aken, Bequencing of Brassica Oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOGIX86TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris
                                                                                                                                                                                                                                                                                                     MetMetGlnProGlyArgValSerLeuValLysAspArgAlaAlaArgTyrAlaAlaAsp
                                                                                                                                                                                                                                               HisGlyLeuAspGluSerPheLeuValAsnLeuTyrAspValIleIleThrGluMetCys 85
                                                                                                                                                                                                                                                                             GAGCTTGAACAGAAAAACACCGATCTCGAGAGTGAGAGGGGCTTCA---CTCGCTGCCCCG
                                                                                                                                                                                                                                                                                                                                                               ArgargargIleaspLeuGlyValargIlealaargTyrLysSerargHisGlyValPro
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                                                                                                     ATTCGTTCTCGAGAGGATCGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center Drive, 301-838-3523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BOGI"
/note="Vector: pHOS1; Site_1: BstXI; 2-3
genomic DNA inserted into pHOS1 using Bst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                         568
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                                                                                                                                                                                       76
                                                                                                                                                                                                                                                               56 LysAspArgAlaAlaArgTyrAlaAlaAspHisGlyLeuAspGluSerPheLeuValAsn
                                                                                                                                                                                                                                                                                                                                                           36 AlaArgTyrLysSerArgHisGlyValProMetMetGlnProGlyArgValSerLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LeuLeuAspThrValArgArgArgIle------AspLeuGlyValArgIle
627 bp mRNA line 010625AAYA002796HT (AAYA) Royal Gala 126 DAFB t domestica cDNA clone AAYA002796, mRNA sequence. CN894351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14228 row: j column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Location/Qualifiers
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU915943.1
EST.
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                                                                                                                                                                                       LeuTyrAspValIleIleThrGluMetCysArgValGluAspLeuValMetSerArgGlu
                                                                                                                                                                                                                                   CGGCAGAGGGCAGAGAGAGGCTGCAGAACACAGGATGTCTCTAAATGCTCTGGAAAAC
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/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2:
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2:
Cloned unidirectionally. Primer: Oligo dT. Average
size 2.2 kb. Constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="oocytes"
/lab_host="DH10B (phage
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/db_xref="taxon:8355"
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Gala 126 DAFB fruit
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                                   TITLE
                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      31 ---LeuGlyValArgIleAlaArgTyrLysSerArgHisGlyValProMetMetGlnPro
            1 (bases 1 to 529)
Holt,RA, Lin,J.-J., Murphy,S.D., Evans,G.A., Kraft,CCharlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Facility
The Horticulture and
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                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                Anopheles gambiae (African malaria
Anopheles gambiae
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19600449718069
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EST.
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                                                                                                  Anopheles.
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Mt Albert Rd, Mt Albert, Auckland, New Zealand
100 64 09 815 4200
100 64 09 815 4201
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Holt R.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev stage="126 days after full bloom" /clone_lib="(AAYA) Royal Gala 126 DAFB fruit cortex" /notee="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
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75.50
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43.33*
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5', mRNA
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45 w. Gude Dr., 1
Tel: 2404533151
Fax: 2404534580
                                                                                                                                                                                                                                  BOHTE10TF BO 2 3 KB Brassica genomic survey sequence.
BH654655
                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicots) rosids; eurosids II; Brassicales; Brassicaceae; Brassicaceae; I (bases 1 to 644)
                                                                                                                                                                     Brassica oleracea
Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                           Contact: Chris Town
                                                          Whole genome shotgun sequencing 
Unpublished (2001)
                                                                                                                                                                                                    BH654655.1
GSS.
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Seq primer: M13 Reverse.
                                                                                       Town, C.D., Van Aken, S.,
                                                                                                                                                                                                                                                                                   BH654655
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301-838-3523
           Medical Center
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference Reagent Resource Center (www.malaria.mr4.org)"
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/clone="19600449718069"
/dev_stage="Adult"
/lab_host="DH10b"
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/mol_type="mRNA"
/strain="RSP-ST (Reduced susc
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                                                                                                                                                     Tracheophyta;
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BH248862
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                                                                                                                                                       Brassica oleracea
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GSS.
                                                                                                                                                                                                                                 BOGAM09TF BOGA Brassica oleracea genomic clone
                                                                                                                                                                                                                                                 BH248862
                                                  Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOGAM09TR
                                                                  Dases 1 to 756)

1 (bases 1 to 756)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                                      Brassica oleracea
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is from a doubled haploid
Medical Center Drive, 301-838-3523
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                                       Chris
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/note="Vector: pHOS1; Site_1: BstXI; 2-3
genomic DNA inserted into pHOS1 using Bst
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/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHTE10"
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 312)
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W., Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T., Zon,L.I. and Chen,Z.
                                                                                                                                                                                                                                                                                                                                                                                                              312 bp mRNA
RK354A2F12.T3 Zebrafish Kidney Marrow cDNA
clone RK354A2F12 5', mRNA sequence.
CD602770
State Key Lab for Medical Genomics Shanghai Institute of Hematology, Ruijin Hospital Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China Tel: 86-21-64740490
                                                                                                    Gene Expression Profiling in the Zebrafish Kidney Unpublished (2003) Contact: Chen Z.
                                                                                                                                                                                                                                                                                                                         Danio rerio (zebrafish)
Danio rerio
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Class: shear
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DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301-838-0208
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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/clone="BOGAM09"
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Contact: Chen Z.
State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 325)
Song, H.D., Mu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T., Zon, L.I. and Chen, Z.
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                                                                                   Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue Unpublished (2003)
                                                                                                                                                                                                                                                               CD602824.1 GI:31784176 EST.
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/clone lib="Zebrafish Kidney Marrow cDNA library"
/clone="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
Site 2: EcoRI; Total RNA was extracted from the kidney
tissues of mature zebrafish. The poly (A)+ RNA fraction
was separated from total RNA by oligo (dT) cellulose
chromatography. Library was initially constructed in the
lambdaZAP Express vector (Stratagene) and in vivo excise
into pBS-CMV vector."
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/db_xref="taxon:7955"
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/mol_type="mRNA"
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                                                                          Tyler,B. Not Published Tyler,B. Not Published Unpublished (2003) Contact: Tyler B
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Fax: 86-21-64743206
                                                                                                                                                               Phytophthora.
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                   1880 Pratt Dr., B.
Tel: 540-231-7318
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    bmtyler@vt.edu
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/db_xref="taxon:7955"
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Query Match:
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264 GACGAGGAGAGCGGCCTGGAGTACGGCGAGGTGCCGAC---GGAGAAGGACTGGCGCGC 320
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BACKWARD: M13 reverse 17mer at 5' end
Plate: 002 row: F column: 03
Seq primer: M13 reverse 17mer at 5' end
High quality sequence stop: 535.
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/mol_type="mRNA"
/db xref="saxon:67593"
/clone="sMY002F03"
/tissue_type="mycelium"
/cell_line="p6499"
/dev_stage="mycelium"
/clone_lib="Aggriculture Canada Phytophthora sojae EST project_sMY"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
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ALIGNMENTS

Query Match	FEATURES SOUICE ORIGIN			COMMENT	REFERENCE AUTHORS TITLE	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BD178315 LOCUS DEFINITION
tch 100.0%; Score 969; DB 6; Length 969;	producing the same CC and novel biosynthetic gene FH Key Location/Qualifiers CDS (1) . (966): Location/Qualifiers 1. 969 /organisme="Streptomyces venezuelae" /mol type="genomic DNA" /db_xref="taxon:54571"	PI MURAKAMI PC C12N15/61,C12N1/15,C12P17/14//(C12N1/15,C12R1:645),(C12P17/14, PC C12R1:645) CC Transformant producing PF1022 substance and process for CC	PD 03-0CT-2002 PD 03-0CT-2002 PD 03-0CT-2002 PD 22-MAR-2002 PD 22-MAR-2002 PD 22-MAR-2001 PD 082227 PR 22-MAR-2001 PD 082227 PR 22-MAR-2001 PD 082227 PI XOJI YANAI,NAOMI SUMIDA,MANABU WATANABE,TATSUKI MORIYA,TAKESHI	IJI TSU	1 (bases 1 to 969) 1 (bases 1 to 969) Yanai,K., Sumida,N., Watanabe,M., Moriya,T. and Murakami,T. Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene		

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                                                        CAGGACCACTGCCAGGAGCTGTTCCGCACCCTCCACCGCACCGACGACGACGAAGGCGAGAAG
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Matches 969; Conserv
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MEIJI SEIKA KAISHA LTD, KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA, MANABU WATANABE, KOICHI MIYAMOTO,NAOKI MIDO,TAKESHI MURAKAMI OS Streptomyces venezuelae PN WO 0123542-A/3

PD 05-APR-2001

PF 29-SEP-2000 WO 2000JP006783

PR 29-SEP-1999 JP 99P 276314

PI KOJI YANAI, KAORU OKAKURA, SHOHEI YASUDA, MANABU WATANABE, KOICHI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI PI NAOKI MIDO,TAKESHI MURAKAMI NAOKI MIDO,TAKESHI MURAKAMI
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Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Yanai,K., Okakura,K., Yasuda,S., Watanabe,M., Miyamoto,K., Mido,N.
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C12N15/09,C12N5/10,C12P21/02,C07K11/00//(C12P21/02,C12R1:645)
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/mol_type="genomic DNA"
/db_xref="taxon:54571"
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Pred. No. 5.6e-66;
0; Mismatches 0;
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                                                       Direct Submission
Submitted (01-AUG-2003) Koji Yanai, Meiji Seika Kaisha, Microbiological Resources and Technology Laboratories; Odawara-shi, Kanagawa 2500852, Japan (E-mail:koji yanai@meiji.co.jp, Tel:81-465-37-5106, Fax:81-465-37-6397)
                                                                                                                                                                                                                                                                                                             Streptomyces venezuelae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                Nat.
                                                                                                                                                                                                                                          engineered with
                                                                                                                                                                                                                                                          Murakami,T.
Para-position
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                                                                                                                                                      Murakami
                                                                                                                                                                 Yanaı,K.,
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nai,K., Sumida,N., Okakura,K.,
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/organism="Streptomyces venezuelae"
/mol_type="genomic DNA"
                                              Location/Qualifiers
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                                                                                                                    Seika Kaisha,
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Streptomyces venezuelae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 14159)
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St, Halifax, NS B3H 4J1, Canada
Sequence update by submitter
On Jun 5, 2001 this sequence version
Location/Qualifiers
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The gene cluster for chloramphenicol biosynthesis in Streptomyc venezuelae ISP5230 includes novel shikimate pathway homologues a monomodular non-ribosomal peptide synthetase gene Microbiology 147 (Pt 10), 2817-2829 (2001)
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Direct Submission
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GQEIGPETSIFDAGGSSLAMIQIQVKLSDAVGEEAVEAARADDYDFAPAAFLRHLRG
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ADFLDLSAATUTAVGDPYSRSKLISEBEYVNTLAVLGCAVSHYRPGLYYGHRPEDRHHL
KDDWFTALLETARRVCAMPRLSGHVPVCDVGTLADTLLGRPDANFGTADGASRTPDSR
KDDWFTALLETARRVCAMPRLSGHVPVCDVGTLADTLLGRPDANFGTADGASRTPDSR
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STREPTOGRAMINES AND METHOD FOR PREPARING PATENT: WO 9601901-A 2 25-JAN-1996;
RHONE POULENC RORER SA (FR)
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Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F.,
Barriere, J., Debussche, L., Famechon, A., Paris, J. an
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Streptomyces pristinaespiralis
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetacede, Streptomyces.
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2 from Patent WO9601901:
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/mol_type="unassigned DNA"
/db_xref="taxon:38300"
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Sequence 2 :
AR198354
AR198354.1
                                                                                                  1 (bases 1 to 888)
Blanc,V., Thibaut,D., Bamas-Jacques,N., Blanche,F., Crouzet,J.
Barriere,J.-C., Debussche,L., Famechon,A., Paris,J.-M. and
Dutruc-Rosset,G.
Streptogramins for preparing same by mutasynthesis
Patent: US 6352839-A 2 05-MAR-2002;
Location/Qualifiers
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1 (bases 1 to 2888), Blanc, V., Thibaut, D., Bamariere, J., Debussche, L., Dutruc-Rosset, G.
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/mol_type="unassigned DNA"
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Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F., Crouzet, J.,
Barriere, J.-C., Debussche, L., Famechon, A., Paris, J.-M. and
Dutruc-Rosset, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and analysis of genes from Streptomyces pristinaespiralis encoding enzymes involved in the biosynthesis the 4-dimethylamino-L-phenylalanine precursor of pristinamycin I Mol. Microbiol. 23 (2), 191-202 (1997)
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Blanc, V., Gil, P., Bamas-Jacques, N., L
Schleuniger, J., Bisch, D., Blanche, F.,
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4740 bp DNA linear BCT 07-MAR-Streptomyces pristinaespiralis 4-dimethylamino-L-phenylalanine precursor biosynthesis (papA, papC, papB, papM) genes, complete
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GAPAGPLGEQITYDVADRAVRVKDGSGGETRRPGTLFDHLHEILARALHATGLFPEF
NLGYVGYLGYETKADSGGEDAHRGELPDGAFWFADRMLALDHEOGRAWLLALASSTRAP
ATAPAAERWLTDAARTLATTAFRPFFTLLPDDQLPALDVHYRHSLPRYRELVEECRRL
                                                                                                                                             ITDGETYEVCLINMLRVPGRIDPLTAYRALRTVS PAPYAAYLQFPGATVLSSS PERFL
RIGADGWAESKPIKGTRPRGAGPAQDAAVKASLAAABEKRRSEULMIVDLYRDDLGQVC
DIGSVHVPGLFEVETYATVHQLVSTWEGRLAADVSRPBAVRAAPFGGSWFGAFKVRD
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                                                                                                                                                                                                                                                                                                                    /gene="
68. .22
                                                                                  /gene="papC"
                                                                                                                            devremlikaQttlaalrQahagatasdrellagslr'
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68._.2227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/mol_type="genomic DNA"
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cuai Jules Guesde, B. P.
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                                                                                                                                           GGCATGGCCGCGGAGCTCGCGGCCCACGCCCCCCGGCGTCCAGCACGTGGGCCTCAACCCC
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GARVVEMPARRHDELTAAQQAATHAAVLAFGLGLGELSVDVGALRDSAPPPHLAMLAL
LAR I AGGTPEVYFD I QAANPGAPAARQALGRGLVRLGQAVERGDEETFAALFAELRGV
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Cercopithecine l
AY714813
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Complete genome sequence of Cercopithecine herpesvirus 2
comparison with other simplexviruses
virology (2004) In press
2 (bases 1 to 150715)
Tyler,S.D., Peters,G.A. and Severini,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-AUG-2004) Health Canada, National Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory, 1015 Arlington St.,
Location/Qualifiers
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dense

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AI FINNKRCVEHEFGNLMKALEGGLFLTEHMOFVDER FVVPESE TINDANLFGWIRLF
SSHKEVSAYMARLHAHLKVAREGEFVVFTLPLLTFVSTKAFEBYRELTHODALTVEKW
I AANAGR I TNYSOS ODODAGR VRFEVHS KOOLVVARNDVTYVLNS OI AVTTRLRKLVF
GFGGTFRS FEAVLRDDS FVKTQGEMLVEF XY FLSKIL I FGGLIHLFYNFLLR PGLDAKK
RARAYERMGALTTELLALGAGEAEGABOAP PAAGERAFDFKTLGARAADDAFFPEDD
LDVVFAGLSEOELDLFY CHYVPEOPDTTAAVHAQFGLLKRAFLGRYHILRELFGEAFE
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15162. .1719
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AAAGLAELLEESPLPYVVLRDQHGFMSVVNTNVSEFVESVEARELAMATNADYGISSM
LAMTITRSQGLSLDKVAICFTPGNLRLNSAYVAMSRTTSSEFLRMNLNPLRERHERDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAAPSGEEETAAAALRQAVAGDRDLVGVAEAISHQALLRMACE VRQAAGRDVRFTATGVSRVDVTPDRILRFALDGGPADALTASEDYFARCKQAAHRGF AFAVVLAGEDHVYSLCVPPLVLPHRLSVFRPERLEDFELACLLMYLENCFRAHATASA FVKLSAWLAAVGRRTSPFDRVRCLLLRSCQMMLNTLMFWUHVBFFDDRYVLPHWCMAR FVKLSAWLAAVGRRTSPFDRVRCLLLRSCQMMLNTLMFWUHVBFFDRVRAAFBFAGLA YLLDHNPPFILTALFRAAPSRVFRLPVRPGTNLECVAYNPDGVLSGGWAAEDFRAGLA
DPLALAAHVAARPAARLAWARLAAIQDTPQCASAASLAVRIDTGTARFAREYTTLTFF
                               /translation="MGEDGLAWAEESVCAVTLYAAWLPPRTRDRLHALLYLLCRDARG
DAVARFAEVAVASSELQAFYGPGEISAAGAVAAARAAASPAAAPLETLNDPALWRALY
ASALAALEREVGGAPLFVPARVGRDPRTGLVARIEAAPGGRPVAPRGAALGVDAQVAT
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complement(18213.
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SFQHQYVPSYAQDLERLSRLMEHELLRCFKI SRHTNNQGRETAI FYSSGAI ALFVAPY
FADVLRAP I PGALI TGPSGVLGEEELMEAI FKKTRVQTYLTDLAALFVADVRHAARRR
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15162. .17198
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IERVRELAGIRLEPARVPRPQMFRDVAALETPADLPLREFPFAVTLITGNAGSGKSTC
VQTLNEVLDCVYTGAYRIAAQMYVYLISGAFISRPINTIFHERGFRGHVQAQLGAP
YALASNPASVEDLQRRDLTYYWEVIADITRRAVAAGGGTEDGRGEFRALAALERTMGL
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/protein_id="AAU88070...
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/product="component of he/protein_id="AAU88073.1"
/db_xref="GI:52843282"
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/protein_id="AAU88072.1"
/db_xref="GI:52843281"
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17149. .18039
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                                                  GCTGGCCCCGGCCCCGAGCCCCCGCCCTGGGGGGGCGCGACCCCGGACTGGGACCC
                                                                                                  CTGGGCCGCCGGCCGACACGCTGCTCGCCGACGCCGAGGACGCCGCCGCCCTGGA
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QWHLTYNAA PGALP I PAFLGBEFEPRGAGAVDHFAVLGF PGWPTLKV PAGAAAVPAAA
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AGPAAVGERARALEGVAGEALAGGGLLRPEEPPPSLELEGIYTHAVLWSQTGAWFWNA
RTDADRLEGFPQGFDAYAAAAATRALRGAVAAYABGAGAEKARLAAEEALDGLVLE
AFARRLDAEYWAVAEGPSDPGDTPPAAALRGGGALLDSERHSRRVVRVCGGPDGGSVAV
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SOURCE
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AY714813/c
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyler,S.D., Peters,G.A. and Severini,A.

Complete genome sequence of Cercopithecine herpesvirus 2 (SA8) and comparison with other simplexviruses
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Cercopithecine herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology (2004) In press
2 (bases 1 to 150715)
Tyler,S.D., Peters,G.A. and Severini,A.
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Cercopithecine herpesvirus
AY714813
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1 (bases 1 to 150715)
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complement (8315. .8320)
9469. .10167
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                                                                                                                                                                                                  EYSRTRRCLGRDTPGLFDEPRLRSPLSAPGDEAAPQPFSPAAPTSSAPPARRDRKPRF
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/gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="complexes with gH; involved
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virus 2, cc
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complete genome.
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11130. .11813
/gene="UL3"
11130. .11813
/gene="UL3"
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complement (11897. .12511)
/gene="UL4"
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LAMTI TRSQGLSLDKVA I CFTPGNLRLNSA YVAMSRTTSSE FLRMNLNPLRERHERDD
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                                                                                                                                                                                                                                      VISGHILSALRDPEVLIVY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELANPLTARLMAEYERRCKAEEVLPPREDVFSWTRYCTPDEVRVVIIGODPYHQPGQ
AHGLAFSVRPGTPAPPSLRNILTAVRNCCPEATMSGHGCLEKWARGGVLLLNTTLTVR
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                  note="role in DNA cleavage/packaging"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="UL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (12536. .15163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APDAPSPPAVSPASAETGAAADLLVEVMKEIOLSPTLGFGPCDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAU88069.1"
/db_xref="GI:52843278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="UL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nuclear bodies"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11809. .11814
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/product="uraci1-DNA glycosylase"
/protein_id="AAU88067.1"
/db_xref="GI:52843276"
                                                                   gene="UL6"
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codon_start=1
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GCCGGACGCCTGCCTGGTGGGCGACGTCACCGCGCCGGGCCCGAACTCGCGGCCGCCCT
                                                                                                                  GCTGCTGCGGGAGGCGGCAGCCGCACGCTCGTCGTCGACCTCGTACCGCCGCCGGGACG
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                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="component of helicase-primase complex"
/protein id="ANUB8073.1"
/db_xref="di="CS843282"
/db_xref="di:52843282"
/db_xref="di:52843282"
/db_xref="di:52843282"
/db_xref="MGEDGLAWAEESVCAVTLYAAWLPPRTRDRLHALLYLLCRDARG
/translation="MGEDGLAWAEESVCAVTLYARIEARGAPAAPLETLNDPALWRALY
ASALAALEREVGGAPLFVPARVGRDPRTGLVARIEARGAFVAPARGAALGVDAQVAT
ASALAALAHCAREVARALAWARLAALAIOUTGCASSLAVRIDTGTARFAREXTTLTFP
PVRKEGAVGDVFEVREAVLR PRGHAQAVTARVLVPRGYEYFAVRAEGFSAPALVALFR
QWHLTVHAAPGALPPIFAFLCPEFEPRGGAVDHFAVLCFPGWPTLKVPAGAAAVPAAA
LTAHAELAGAWPAAGARALAPARLWAAAAAGAPGRLSPATATFGLIRLDPPAVIG
PVCLARFRFPGCIEARLAAALCGLGLEERADPRDPLARGARCWRALAADAREWARAVAA
LALAEARECCPAFARVLDGVVAAVGLRLEAAAGDVDLAVCGNEGASLWGVLNVDPQGA
AGPAAVERARAALEGVAGEALAGGGLLKPEEPPSSLELEGIYTHAVLWSQTGAWFWNA
AGPAAVERARAALEGYAGEALAGGGLLKPEEPPSSLELEGIYTHAVLWSQTGAWFWNA
AGPAAVERARAALEGVAGEDLTPPAAALRGALAGEALDGIVLE
AFARRLDAEYWAVAEGPSDPGDTPPAAALRGALAGEACHATAAEEALDGIVLE
AFARRLDAEYWAVAEGPSDPGDTPPAAALRGALAGLMGEDGGFAYPFEERFLFIFP
POLYFPELVLPPIDCAHHLRDVLAEAEBAVLRGALAGLMGEDGGFAYPFEERFLFIFP
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/gene="UL7"
17149. .18039
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RLVRRYGGAPDADVAAVAERVEPTIWRGALRASLLDFARGLADCEAQCGFGGSVGFSRY
IDWLMCLGLVEVMRREREGEVTORLEAFLAGHALPRIDLATVGGAVERAA PFLIRALARA
FDSAHLADVJRVCLFYHFRRGEWRVEDPAGGRGGECVVLWFPLWAGDRLLFDSFMQRL
FDSAHLADVJRVCLFYHFRRGEWRVEDPAGGRGGECVVLWFPLWAGDRLLFDSFMQRL
SHEIVACAALREHARVCRVRINAASVKVLLGRKWDGDRGFAGAARAVSRALGEDDASRA
GSAASRLVRLI INMKGHRHIGDINDTVRAYLDEAGGHLMSATVDPALFGFGRAAGAG
GSAASRLVRLI INMKGHRHIGDINDTVRAYLDEAGGHLMSATVDPALFGFGRAAGAG
GRAAGGADPAGFROQOLRQAFOTSVVNNINGHLEGYINNLFGTIERLRETNTDLATOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="UL9"
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AWWASDAPKTQTAALFYRFV"
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AFAVVLAGEDHVYSLCVPPLVLPHRLSVFRPERLEDFELACLLMYLENCPRAHATASA
FVKISAWLAAVGRRTSPFDRVRCLLLLRSCQWMLNTLMFMVHVEPFDDRYVLPHWCMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="capsid protein"
/protein_id="AAU88072.1"
/db_xref="GI:52843281"
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SFQHQYVPSYAQDLERLSRLMEHELLRCFKI SRHTNNQGRETAI FYSSGAI ALFVAPY
FADVLRAPI PGALITGPSGVLGEEELMEA I FKKTRVQTYLTDLAALFVADVRHAARRR
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/protein_id="AAU88071.1"
/db_xref="GI:52843280"
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                                                                                                                                                                                                                                                                                                                                                                                     Score 128.4; DB 14; Pred. No. 0.012;
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., B. Hmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Drager, H., Dugan-Rocha, S., Durbin, K.H., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Direct Submission
Submitted (25-JUN-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Bavlor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                         * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 16 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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be preserved.
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Consensus quality: 128020 bases at least Q40
Consensus quality: 129713 bases at least Q30
Consensus quality: 130554 bases at least Q30
Consensus quality: 130554 bases at least Q30
Estimated insert size: 129513; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
Project Trform.
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20661
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85078
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18888
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14451
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10778
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8093
8193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DN
/db_xref="taxon:7668"
/clone="R3-32A21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Strongylocentrotus purpuratus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136753:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85077:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47107: gap of 64347: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9664:
10777:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18987:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 124;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 404;
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g of 15795 bp in
f unknown length
g of 17240 bp in
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unknown
of 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 1113
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length
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3365

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270

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RESULT 13
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KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                           Bouck, J., Bowle, S., Bireva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., David, R., Dugan, R., Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earlhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Becotto, M., Earlhart, C., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Ganaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Jodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Jieu, J., Korvah, J., Kovar, C., Kralsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kralsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kralscon, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kralscon, E., Kally, S., Martin, R., Martin, R., J., Lux, J., Lux, J., Lucler, A., Lucler, R., Luna, R., Ma, J., Lousseged, H., Lozado, R.J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux, J., Lux
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SEQUENCE, 16 unorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus
                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus
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16 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG 25-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3777
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AUTHORS
                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 ... - Worley, K.C.
Direct Submission
25-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUN-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.
NOTE: This is a "working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 128020 bases at least Q40
Consensus quality: 129713 bases at least Q30
Consensus quality: 130554 bases at least Q20
Estimated insert size: 129513; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Center clone name: R3-32A21
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Danchin,A. and Pascal,G.
Direct Submission
Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kc
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yuen, K.Y., Pascal, G., Wong, S.S., Glaser, P., Wc Cai, J.J., Cheung, E.Y., Medigue, C. and Danchin, Exploring the Penicillium marneffei genome Arch. Microbiol. 179 (5), 339-353 (2003)
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AL684264.1
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Penicillium marneffei
Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; mi
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Similarity 45.6%;
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GCTCGGCGGCAGC---CCCGAGGTGTACGGGGACATCCAGCGGTCCAACCCCCGGGCGGC
                                                   GACGCACGCCGTGCTCCTCCTTCGGGGCTCGCCCTCGGCCTCGGCGTCGACGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Penicillium marneffei"
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Pred. No. 0.45;
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Cercopithecine herpesvirus 1 strain
AF533768
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (31-JUL-2002) Department of Biology, University, 24 Peachtree Center Ave, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete sequence and comparative analysis of the genome of herpes B virus (cercopithecine herpesvirus 1) from a rhesus monkey J. Virol. 77 (11), 6167-6177 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecine herpesvirus 1 (monkey B virus)
Cercopithecine herpesvirus 1
Viruses, dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 156789)
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APAPAGNPAFIVIGDSPPASPRRPSGAAAPPVVPVAPRPRPAAEPPAPAPGAAPRQPA
                                                                                                                                                                                                                     2194.
                                                                                                                                                                                                                                                  224.
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                                                                                                                                                                                                                                note="terminal copy of large repeat region"
                                                                                                                                                                                                                                                               'note="a sequence"
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GA 30303, USA
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10711. .11394
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GQAHGLAFSVRPGTPTPPSLRNILAAVRNCCPDAELAAHGCLEKWARGGVLLLLNTTLT
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9072. .9746
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KEVSAYMARLHAHLKVAREGEFVVFSLEVHSKAFDEYRELTHGPALTVEWI AA
NAGRITMYSGSGDQDAGRARLEVHSKOOLVVARNDVTYVLNSQIAVTTGPLKKLVFFSF
GTERSFEAVLRDDSFVKTQGEMLVEFAYQFLSRLIFGGLIHFYNFLLRPGLDAARRAR
AYEMGALTRELLSLGATGAGPATFGDGAASGGGESASAAFGARAFDFKTLGARATDE
AFFEDDLDVVFAGLMEGLDLFYCHTYVEQPETTAAVHAQFGLLKRAFLGRYHILE
LFGEAFEGAPGTYVDNVTFRGCEVMIGSMRGGLMSVALQTDSYTLTGFTYARVYAFA
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SWWSSDAPKTQTSALFYRLV"
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ACALVALEREVGRAALFAPARVAWDPRTGLVARIEGLPDGRSPAPRAAALDVNAQIAT
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DYGISSMLAMTITRSQGLSLDKVAICFTPGNLRLNSAYVAMSRTTSSEFLRMNLNPLR
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complement(12172.
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/protein_id="AAP41426.1"
/db_xref="GI:30844250"
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QWYLTVHAGPGALPPIFAFLGPE$FEPRGGAVDHFSVLGFPGMATLKVSGGAAAAPPAA
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PWPREVLALATIDEVRREYPAVARTLDGIVSAVGYGLEKAAGAVDWAAVCGDGGGRVWGV
LNVDPRDAAGAGAAAAAAERAAALAASASEALAGWGLRLDAPPPLVLEGTYTHAVLW
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Job time : 4458.25 secs

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Maximum Match 100%
Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        GenCore version 5.1.6 (c) 1993 - 2005 Compugen
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agrochemicals.

Claim 15; Page 67-70; 83pp; Japanese

Transformant producing secondary metabolite modified with functional group e.g. benzene with nitrogen-containing substituent at para-position, PF1022, with ease at low cost, for application in pharmaceuticals and

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                                                                    The present invention relates to transformants capable of producing PF1022 substance derivatives. These were obtained by transferring a gen participating in the biosynthesis pathway from chorismic acid to paminophenylpyruvic acid (biosynthesis gene) into a phenylalanine-requiring host derived from an organism producing the PF1022 substance. The transformants are producing PF1022 substance derivatives by fermentation, for use as pharmaceuticals or veterinary drugs. The prese sequence is a substance PF1022 coding sequence from Streptomyces
  Sequence
                                                                                                                                                                                                                                                                                                                                                        Novel biosynthesis gene-transferred transformants for producing PF1022 substance derivatives by fermentation, as pharmaceuticals or veterinary drugs with anthelmintic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substance PF1022; biosynthesis; transgenic; chorismic acid; anthelmintic; phenylalanine; p-aminophenylpyruvic acid; pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                             Matches
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Meggers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for producing protein comprising unnatural amino acid has translation system comprising orthogonal tRNA and orthogonal aminoacyl tRNA synthetase.
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06-FEB-2002; 2002US-0355514P
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                                                biosynthesis; p-aminophenylalanine;
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Mismatches

Indels Length 12391;

18;

Gaps

Score 913.8; Pred. No. 1.2 Ç

DB 8; .2e-106; .es 17;

3346 <u>ن</u>

2627 T; 0 U; 0 Other;

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Composition useful for producing protein comprising unnatural amino has translation system comprising orthogonal tRNA and orthogonal
                                                                                                                                                                                                             19-APR-2002; 2002WO-US012465
                                                                                                                                                                                                                                                                           WO200285923-A2
                                                                                                                                                           2001US-0285030P
2002US-0355514P
                                                                                             Anderson
                                                                            nderson JC,
Pastrnak M,
                                                                              Chin JWK,
Santoro
                                                                            . SW,
                                                                                               Liu
                                                                              Zhang
                                                                                                 DR,
                                                                                               Magliery
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aminoacyl tRNA synthetase. acid,

Example 4; Page 124-127; 188pp; English.

The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-tRNA with at least one unnatural amino acid in the translation system and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Aspl2TAG mutant of chloramphenical acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse acid is provided exogenously. The translation system is a cell and the unnatural amino acid is biosynthesised by the cell. The presents sequence represents a plasmid for use in the biosynthesis of p-aminophenylalanine (pAF) in vivo

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AGGGACGGGCCGGGCGCACGCCCTGCTGCGGCCTCGTCGAGGGCGGCGGCGGCGGCAGGCCC
                                                                                               AACCCGATGTTCGCCCCCGCCGCCGGCATGACCGGCCGACCCGTGGCCGTCGTCACC
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         Blanc V,
Barriere
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                                                  08-JUL-1994;
                                                                     04-JUL-1995;
                                                                                                      WO9601901-A1
                                                                                                                                       mat_peptide
                                                                                                                                                                Streptomyces pristinaespiralis
                                                                                                                                                                                                                    Streptomyces
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                  Thibaut D,
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                                                                     95WO-FR000889
                                                                                                                                               Location/Qualifiers
                                                                                                                                /*tag=
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New streptogramin B derivs. useful as mutants of Streptomyces having altered biosynthesis.
                   altered
                                   antibiotics - produced
                   genes
                      for
               s - produced by new
streptogramin B
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Claim 18; Page 105-106; 146pp; French

The papA and papM genes of S.pristinaespiralis are involved in the biosynthesis of 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor for pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papC) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The PapC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DMPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The second open reading frame (constant) to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-deoxy 4-aminoprephenate acid. Disruption of the papB gene product is the used to produce strains of S.pristinaespiralis which are unable to produce the antibiotic pristinamycin I but which may be able to produce con the condified forms of it

Similarity TTCCCCCGCAGCGTCGTCGTCGGCGGCAGCGGGAGCGGGGCGGTGGGCCGCATGTT----CGCCGGG CTGCTGCGGGAGGCGGCAGCCGCACGCTCGTCGACCTCGTACCGCCGCCGGGACGG TTCGGGCGTTGTGTGGTGGGCGGGGGGCCGGTGGGGCCGCATGTTCAGCCACTGG 27.9%; ilarity 58.8%; Conservative 73 A; 254 C; 0; Score 270.8; DB Pred. No. 7.4e-26 0; Mismatches 33 428 G; 133 7.4e-26; ies 337; T; 0 2 ₽; 0 Indels Length Other; ω •• Gaps 78

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CCCGTGACCCGGCTCATGCGGCGGCGGCGCGCTCGCCGACACCCCTGTCCGGTCCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGACGCGGACCTCGTCCTCGCTGCTCGCCGTACACGGACGACGTGGCCCTCAAGGCCCGTGGCG
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ACGGCACCGCCCCACCAGGTGCTGCTCGCCCTCCTGGCCCGTGTGCTCGGCGGCAGC
                                                 GTGCTGGCCTTCGGGCTGGGCCTGGGTGAGCTGTCGGTGGACGTGGGGGGCGCTGCGGGAC
                                                                                  CTCCTCTCCTTCGGGCTCGCCCTCGCCTCGGCGTCGACGTCCGGGCCCTGGCCGCC
                                                                                                                                              GGGCCGGGCGTCACGGCCCTGCTGCGGCGTCGTCGAGGGCGGCGGCGGCAGGCCCGTACGG
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RESULT 6
AAT5928/c
ID AAT592
XX AAT592
XX Strept
XX Strept
XX Strept
XX Strept
XX DAPAPA
KW DAPC;
XX DAPC;
XX PT CDS
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                               Example 1; Page 102-104; 146pp; French
                                                                             New streptogramin B derivs. useful as antibiotics mutants of Streptomyces having altered genes for s
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pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papC) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The PapC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino phenylpyruvate during DMPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is likely to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-deoxy 4-aminoprephenate. Disruption of the papB and papC genes can be used to produce strains of 5.pristinamycin I but which have belt to produce new, modified forms of it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthesis of 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor
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390 A; 1319 Ç; 897 G; 282 T; 0 U; 0 Other; DB 2; Length 2888;

Similarity GTGCTGGCGGGGGTGATGCGGCCCGGTGCGGTGCTCGCGGACACCTTGTCGGTCAAGAGC GCGGCGGCGGACGTGGTGGTGGCGGCGGTGCCGGAGCCGGTGGCGTGGGAGGCGGTGGAG CGGGACGCGGACCTCCTGCTCGCCGTACACGAGGACGTGGCCCTCAAGGCCGTGGCG GGGGTGCGGGTGGCCGGTGATGTGCGGCGGCCGGGGCCGGAGGCCGGTCGCGGCGCCCTG CTGGTGCGTTCGGGGGGCGGTGGCCGGTGACCTGGCTGGACGTGGCCGGGGCCGGAC CTGCTGCGGGAGGCGGGAGCCGCACGCTCGTCGACCTCGTACCGCCGCCGGGACGG TTCGGGCGTTGTGTGGTGGGCGGGGGGCCGGTGGGCCGCATGTTCAGCCACTGG Conservative 27.9%; 58.8%; 0, Score 270.8; DB 2 Pred. No. 5.6e-26; Mismatches 337; Indels ω --Gaps 1519 1579 246 1639 1699 1759 306 186 126 99

CGGATCGCCGGGCGGCTGCGTGAGGCGGCGGCCGGGGCTGCAGGCGGTGGGGCTGAACCCG 1459 366

ATGTTCGCCCCCCCCCCCCCATGACCGGCCGACCCGTGGCCGTGGTCACCAGGGAC 426

ATGTTCGCCCCCTCGCTGGGTCTTCAGGGGCGGCCGGTGGCGGCGGTGGTCACCGAC

486

GTGCTGGCCTTCGGGCTGGGCCTGGGGTGAGCTGTCGGTGGACGTGGGGGCGCTGCGGGAC 606

ACGGCACCGCCCCCCACCAGGTGCTGCTCGCCCTCCTGGCCCGTGTGCTCGGCGGCAGC 1219

CTGGGCCGGCCTGGTGCGGCTGGGGCAGGCCGTCGAGAGGGGCGACGAGGAGACGTTC croscos de la constanta de la 1039 1099 786

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                                                                                                                                                                                                                                                                                                                         The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
                                                                                                                                                                                                                               acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphyse chronic obstructive pulmonary disease; leukemia; lymphoma; colon cancer; breast cancer; lung cancer; pancreatic cancer
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   Sequence 114955 BP;
                                                                                             colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, well as all types of cancers which may metastasize or have metastasized
                                                                                                                                                              disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides used in treatment of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1997;
09-JUN-1998;
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6071 A; 29417 C; 36712 G; 21328 T; 0 U; 21427 Other
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                                                                         GGCGCGCCCVGGCCGNNHNNNSGGCCCGGCCGGCGCGCCCVGGCCVGCGNNH
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Valla S,
                    WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144,
AAE10149, AAE10150.
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10-APR-2000; 2000GB-00008786.
14-APR-2000; 2000GB-00009387.
                                                                                                            (UYNO-)
(SNTF)
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(DZIE/)
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(SEKU/)
(FJAE/)
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                                                                                  BRAU/
  antibiotics
nystatin polyketide synthas
antibiotics and antifungals
                                                                   SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
STROM A R.
VALLA S.
                                              SB, Sekurova O
, Ellingsen TE,
                                                                                                                         UNIV NORGES TEKNISK NATURVITENSKAPELIGE. SINTEF STIFTELSEN IND TEK FORSK. ALPHARMA AS.
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antibiotic;
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/note= "CDS does not include
complement(59045. .60241)
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6337. .34771
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complement(60238.
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7503. .58687
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1155. .57355
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Sletta H,
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The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence Streptomyces noursei nystatin PKS gene cluster English DNA gene 18

TCGTCGGCGGCAGCGGGCGGTGGGCAGGCATGTTCGCCGGGCTGCTGCGGGAGGCGGGCA Score 115.6; 1 Pred. No. 5.9e 0; Mismatches . 9e-DB 4; 459; Indels Length 125401; 24; Gaps 85 4.

GCGACGTCACCGCGGGGGCCCGAACTCGCGGCCCCCTCCGGGACGCGGACC---TCG CCCTGGACGACGCCGCGCGCCCCCCTGTGGTGCGTCACCCGCGGCGCCGTCGCGG eccecacercercerceaccrceracececceceeaceccecaceccrecreere 28679 202 145 28619

TCGCGGGGGAGGCCCGACCGCCGTCGGGCCAGGCCGCCCTGTGGGGCCTGGGGCCGGGTCG TGCGGCCGGCGCCCCCCCCGACACCCCTGTCCGGACGGGCATGGCCGCGGAGC CCGCGCTGGACCACCCGGACCGCTTCGGCGGCCTGGCCGACCTGCCCGACACCGACG TCCTGCTCGCCGTACACGAGGACGTGGCCCCTCAAGGCCGTGGCCCCGTGACCCGGCTCA 322 262 28799 28739

TCGCGGCCCACGCCCCCGGCGTCCAGCACGTGGGCCTCAACCCGATGTTCGCCCCCGCCG CGCACGCCGCGGGCTGCTCGCCGCGCACCTGGCCGCGC---CGGGCACCGAGGCCGAGA 382 28916 28856

CCGGCATGACCGGCCGACCCGTGGCCGCCGTGGTCACCAGGGACGGGCCGGGCGTCACGG 442 28976

CGGCTCGTCGAGGCCGGCGGCAGGCCCGTACGGC

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TGACCGCCCCGACGCACCACGACCGCCGCGGACACCGAGGCCCTGACG---GCCGAAC

TGGCCGCGCTCGGCGCCCGGATCACCGTCGTGGACCACGACCCCACCGCCCCGGACGGCT 29153 607

TCGCCGCGCTCCTCGACGGACTGCCCGACGACACCCCCGCTCACCGCGGTCGTGTACGCGC 667 29213

CGGAGGCCGACGCCCCCCGGCACCCGCGCGCAGCTGTCCGCCGCACTCGCCCCCGTCA 29273

ACGGCGTCTTCGGGGAACTCCGCCGGCTCATGGGACCGGAGCTCGCGGCGGGCCAGGACC TCGCCGGGCTCTGGGGCGTGCGCGGGCCGGGCCGAGGCCGCGTCCGGCGCCTACCTCG CCCCGGGCGCGCGACGCCCCGGGCATCCCGGGGATGCGACGGCGCCGGGAACCTCG CCGCCCTAGGCGCCCCTCACCGGCCGGCCGCTGGACGCCTTCGTCCTCTTCGGCTCCA 907 847 787 29393 29333

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                                      diseases, pulmonary vasoconstriction, inflammation, including lung acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (CODD), and cancers such as leukemias, lymphomas, carcinomas e. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                             end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide; multiple target; antisense treatmultiple respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                            diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5 -end, the 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1997;
09-JUN-1998;
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chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
   Sequence 114955
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Valla S,
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P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, A
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135,
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) VALLA S.
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BRAUTASET T.
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Similarity 46.9%;
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                                                                                                                                                                                                                                                                                                                    Novel maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansamitocin gene cluster I of Actinosynnema pretiosum, useful as antitumor agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansamitocin general cluster I of Actinosynnema pretiosum, useful as antitumor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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CAGGGACGGGCCGGCCTCACGGCCTGCTGCTGAGGGCGGCGGCGCCAGGCC
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                                                      The invention relates to maytansinoid produced by bacterial host celtransformed with expression vector comprising open reading frame from ansamitocin gene cluster I of Actinosynnema pretiosum. Maytansinoid useful as a potent antitumour agent. The present sequence is A. pretansamitocin gene cluster I polyketide synthase (PKS) gene
                                                                                                                                                                                                                                                                                                         Novel maytansinoid produced by bacterial host cell transformed wi expression vector comprising open reading frame from ansamitocin cluster I of Actinosynnema pretiosum, useful as antitumor agent.
                                                                                                                                                                                                                                              Disclosure; Page 59-61; 160pp; English.
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Matches Query Match Best Local

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Conservative

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Score 111.6; DB 8 Pred. No. 4.2e-06; 0; Mismatches 429

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Indels Length

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/product= "ORF2,
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/*tag= j
                                                                                                                                                                   /product= "Polyketide
extension modules 18 a
nodosus amphK gene"
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extension modules 15, 16 and 17 encoded by S. nodo
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                                                            complement (58756.
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                /*tag= q
/product= "Polyketide synthase m
/product= "Polyketide synthase m
extension modules 3, 4, 5, 6, 7
nodosus by amphC gene"
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complement(61798.
                                                                                                              /product= "Polyketide synthase multienzyme housing extension modules 1 and 2 encoded by S. nodosus by
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66081. .70319
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70366. .79938
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                                                                                                                                                                        /product= "Polyketide synthase multienzymeloading module encoded by S. nodosus amphA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ORF3, hypothetical protein"
/transl_except= (pos:59869. .59871, aa
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27-MAY-2002; 2002WO-IE000071

31-MAY-2001; 2001IE-00000527

(-טמצט) VIND COLLEGE DUBLIN

Caffrey JP;

WPI; 2003-201271/19.
P-PSDB; AAE36116, AAE36117, AAE36118, AAE36119, AAE36120, AAE36121, AAE36122, AAE36123, AAE36124, AAE36125, AAE36126, AAE36127, AAE36128, AAE36129, AAE36130, AAE36131, AAE36132. AAE36128,

Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, uses for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than amphotericin.

Claim 1; Page 52-114; 276pp; English

for producing amphotericin derivatives glycosylated with alternative sugars; amphDII or amphDII gene sequences are useful in engineered biosynthesis of perosaminyl-amphoteronolide B; amphDII or amphDII and amphN gene sequences are useful in the engineered biosynthesis of perosaminyl-16-descarboxyl-16-methyl amphoteronolide B; amphDIII, amphDII and amphDI gene sequences are useful for preparing polypeptides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine. The present sequence is S. nodosus amph biosynthetic gene cluster responsible for the biosynthesis of the polyene antibiotic amphotericin (amph) of Streptomyces nodosus. Polymucleotides of the invention are useful for preparing amphotericin derivatives or analogue antibiotic agents with altered properties and in the biosynthesis of polyketides other than amphotericin, amphDIII, amphDII or amphDI mutants are useful The invention relates to the gene cluster encoding the polypeptides

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Best Local Similarity 46.2
Matches 439; Conservative
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Similarity 46.2%; Pred. No. 4.3e-06;
39; Conservative 0; Mismatches 502; Indels 9;
                                                                                                                                                                                                                                                                                                                                            GGCGCCGCGGCGGGTCTGATCCGCACCGCCCGCACCGAAACCCCGGCCGCTTCGT 83944
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                       CCACTGCCAGGAGCTGTTCCGCACCCTCCACCGCACCGACGACGAAGGCG 955
                                                                  CACCGGCGCACCGGCGGACTCGGCGGCGTCCTCGCCCACCTCGTCACCGAACGCGG
                                                                                                  CGCCCCGGGCCGCCGACCCCCCGGGCCATCCCGGGGGATGCGACGGCGCCGGGAACCT
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CGTCCGCCGGCTGCTCGCCAGCCGCCGCCGGCCGGCCGCCGACGGCG 84234
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Search completed: October Job time : 595,401 secs

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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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US-09-105-537-5

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CGGCTC	GACCTCG GACGTGG	recerses	GAGGCGC TCGGGGC	CCCCGCAGCGTCGTC 	27.9 58.8 vative	9: 1997-03 9: 17 Ver. 2.0 Nyces prist	S, Jean-Marc UC-ROSSET, G ON: Streptog ON: Mutasyn Streptogrami TON UMBER:	GCE1 3, Jean-Claude 4E, Laurent V, Alain	Denis Denis ACQUES, I Franci	g		23673	1272	77536 77536 1288	20235 20235 23673	4257 4257 12001	15872 1403765 4257 4257
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CCCGTGACCCGGCTCATGCGGCCGGGCGCGCGCGCGGCGCGGCGCGGGCGG	GCGGACCTCGTCCTGCTCGCCGTACACGAGGACGTGGCCCTCAAGGCCGTGGCG 246	CGGGGCCCGAACTCGCGGCCGCCCTC 186	CTGCTGCGGAAGGCGGCAACCCGAACGCTCGTCGTCGACCTCGTACCGCCGCCGGGACGG 126	GGTGGGCGCATGTTCGCCGGG 66	3 3; Length 888; 14; 137; Indels 3; Gaps 1;		or Preparing Same By					7,	sequence 98:	Sequence 1, Sequence 1, Sequence 9,	Sequence 3, Sequence 3, Sequence 1,	Sequence 1, Sequence 1, Sequence 11,	

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FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 888
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US-09-987-614A-2
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APPLICANT: BLANC, VERY
APPLICANT: HIBAUT,
APPLICANT: BAMAS-JAC
APPLICANT: BLANCHE,
APPLICANT: BUZZET,
APPLICANT: BARRIERE
                                            Query Match
Best Local Sim
Matches 486;
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Streptogramins And Method TITLE OF INVENTION: Mutasynthesis
                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Streptomyces
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                                                                                         Similarity
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COUZET, Joel
BARRIERE, Jean-Claude
DEBUSSCHE, Laurent
FAMECHON, Alain
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DUTRUC-ROSSET, Gilles
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BAMAS-JACQUES, Nathalie
                                                Conservative
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58.8%;
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                                            Score 270.8; DB 4;
Pred. No. 9.3e-34;
0; Mismatches 337;
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                                            1;
                                                                                                                                                  Sequence 1, Application US/08765907A
Patent No. 6352839
GENERAL INFORMATION:
APPLICANT: BLANC, Veronique
APPLICANT: THIBAUT, Denis
APPLICANT: BANAS-JACQUES, Nathalie
APPLICANT: BLANCHE, Francis
APPLICANT: BLANCHE, Francis
APPLICANT: BLANCHE, Francis
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSSCHE, Laurent
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US-08-765-907A-1/c
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CURRENT FILING DATE: 197-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
TENGRAP. 2888
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TYPE: DNA
ORGANISM: Streptomyces
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BLANCHE, Francis
COUZET, Joel
                        CTCCTCTCCTTCGGGCTCGCCCTCGCCTCGGCGTCGACGTCCGGGCCCTGGCGGCG
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DEBUSSCHE, Laurent
FAMECHON, Alain
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Pred. No. 8.3e-34;
0; Mismatches 337
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RESULT 5
US-08-804-227C-7/c
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
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APPLICANT: DeHOLL, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
COMPUTER: MS-DOS
   FEATURE:
NAME/KEY:
LOCATION:
                                                            FEATURE:
NAME/KEY:
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NAME/KEY:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: THOWAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                              LOCATION: FEATURE:
                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCI(DOS) TE
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SOFTWARE: ASCI(DOS) Text only
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                                             LOCATION:
                                                                                        LOCATION:
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                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                                                                    TOPOLOGY:
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RESULT 6
US-08-804-198-1/c
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Pred. No. 2.9e-08;
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Best Local Similarity
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Patent No.
                                                                                                                                                                                               Matches 438;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P91
TELECOMMUNICATION INFORMATION:
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APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
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NAME: CANTRELL, PAUL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Macinto
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                      GIGGGCGACGTCACCGCGCGGGGCCCGAACTCGCGGCCCCCTCCGGGACGCGGACCTC
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LILLY CORPORATE CENTER
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                                                                                                                                                                                               Conservative
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Pred. No. 2.9e-08;
                                                                                                                                                                                               Mismatches 491;
                                                                                                                                                                                                                        DB 2;
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US-09-105-537-30

(Sequence 30, Application US/09105537A)

PATENT NO. 6265202

(GENERAL INFORMATION:
APPLICANT: Sharman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: CHO, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION UMBER: US/09/105,537Å
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 13842
TYPE: DNA
ORGANLSM: Streptomyces venezuelae
US-09-105-537-30

pikromycin

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RESULT 8
US-09-105-537-5
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and TITLE OF INVENTION UNMBER: US/09/105,537A
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 36778
TYPE: DAY
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Pred. No. 3.4e-08;
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GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-09-22
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CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
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EARLIER FILLING DATE: 1998-05-28
NUMBER OF SEO ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 3.3e-08;
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-141-908-1
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US-09-141-908-1
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CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER APPLICATION NUMBER: PROV. 60/087,080
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                                                      NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 38506
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APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold FILE REFERENCE: 300622002100
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   Sequence 19, Application
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Pred. No. 3.3e-08;
0; Mismatches 515; Indels 2
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FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 199-05-27
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
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                                                         12702 CCTCGGCTGGGGCCTCTGGGCCGAGACCAGCGGCATGACCGGCGAGCTCGGCCAGGCGGA 1276
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RESULT 12
US-10-237-551-193
; Sequence 193, Application US/10237551
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APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538C3
CURRENT APPLICATION NUMBER: US/10/237,551
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 254
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 193
LENGTH: 3957
THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND
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ORGANISM: HSV2
S-10-237-551-193
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Best Local Similarity 46.8
Matches 439; Conservative
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                                                     CCGCACGCCGACGCCCCGCCTGCGCGCGCTGCGCTGCGAGCTGCGGTTCGTGCGCGAC
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                                                                                                     ATGTTCGCCCCCCCCCCCGCATGACCGGCCGACCCGTGGCCGCCGTGGTCACCAGGGAC
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Pred. No. 6.8e-08;
0; Mismatches 484;
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 8
                                                                                                                                                                                                                     Matches 439;
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
TITLE OF INVENTION: AGENTS
FILE REFERENCE: PO1949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                   LENGTH: 154746
TYPE: DNA
ORGANISM: HERPESVIRUS
                                                             151462 GCGGTGCCCGCCGGCTACGGCGCCGCGGGGGTGCTCGCCCCCTGGGGCCCCTGAGCGCC 151521
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Sequence 8, Application US/09827688
Patent No. 6821955
GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,68
CURRENT FILLING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 8
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, COMENCE.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN /
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/ cgnn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

n	Result
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969 915.4 913.8 115.8 115.6 114.8 109.2	Score
0000000	Query Match
969 3305 12391 138203 125401 65140 4569	Query Match Length DB ID
20 14 14 19 19	BB
969 20 US-10-472-587-5 3305 14 US-10-126-927-68 12391 14 US-10-126-927-67 138203 21 US-10-819-306A-1 125401 19 US-10-203-295-35 65140 19 US-10-203-295-1 4569 15 US-10-156-761-7339	ID
Sequence 5, Appli Sequence 68, Appl Sequence 67, Appli Sequence 1, Appli Sequence 35, Appl Sequence 1, Appli Sequence 7339, Ap	Description

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11 24 16 16 11 19 19		15 15 20 20 15 14 14 14 14 16
US-10-158-759-150 US-11-053-576-84 US-11-053-576-84 US-11-053-052-84 US-10-329-079-46 US-10-329-079-34 US-09-758-759-1 US-10-203-295-29 US-10-203-295-29 US-10-156-761-3788	US-09-861-289-5 US-09-860-846-5 US-09-860-846-5 US-09-860-848-5 US-09-988-384B-5 US-09-988-384B-5 US-09-793-708-19 US-10-201-365-1 US-10-468-828-19 US-10-207-562-193 US-10-207-562-193 US-10-207-688-8 US-09-827-688-8 US-09-827-688-8 US-10-939-036-35	US-10-156-761-1 US-10-156-761-3440 US-10-472-587-5 US-10-156-761-4723 US-10-156-761-1 US-10-126-927-68 US-10-126-927-68 US-10-126-927-69 US-10-156-761-6049 US-09-861-289-30 US-09-861-289-30 US-09-886-846-30 US-09-886-848-30 US-09-886-848-30 US-09-886-848-30 US-09-886-881-389-30 US-09-886-8821-30
Sequence 150, App Sequence 84, Appl Sequence 84, Appl Sequence 84, Appl Sequence 46, Appl Sequence 14, Appl Sequence 1, Appli Sequence 29, Appl Sequence 1, Appli Sequence 3788, Ap	55 6 7 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Sequence 1, Appli Sequence 3440, Ap Sequence 5, Appli Sequence 4723, Ap Sequence 67, Appli Sequence 68, Appli Sequence 67, Appl Sequence 6049, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl

ALIGNMENTS

RESULT 1 US-10-472-587-5

```
Sequence 5, Application US/10472587

Publication No. US20040214274A1

GENERAL INFORMATION:
APPLICANT: YANAI, Koji
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APPLICANT: MATANABE, Manabu
APPLICANT: MATANABE, Manabu
APPLICANT: MURAKAMI, Takeshi
ITILE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods for TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods for TITLE OF INVENTION: MURAKAMI, Takeshi
CURRENT APPLICATION NUMBER: B003-1302A/MMC/00144
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/10/472,587
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 40
SOFTWARE: DANA
ORGANISM: Streptomyces venezuelae
FEATURE: DNA
ORGANISM: Streptomyces venezuelae
FEATURE: NAME/KBY: CDS
LOCATION: (1)...(966)
US-10-472-587-5
Query Match
Best Local Similarity 100.0%; Score 969; DB 20; Length 969;
Best Local Similarity 100.0%; Pred. No. 3.4e-192;
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RESULT 2
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Publication No. US20030082575A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Schultz, Peter G
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APPLICANT: Wang, Lei
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Meglery, Thomas
APPLICANT: Mesters, Wiro
APPLICANT: Mesters, Wiro
APPLICANT: Santoro, Stephen W
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APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
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APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: Santoro, Stephen W
APPLICANT: DATE: 2002-04-19
CURRENT APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.1
LENGTH: 3305
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; ORGANISM: Streptomyces
US-10-126-927-68
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Best Local Similarity
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ilarity 96.6%;
Conservative
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Pred. No. 3e-181;
0; Mismatches 16;
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Sequence 67, Application US/10126927

Sequence 67, Application US/10126927

Publication No. US20030082575A1

GENERAL INFORMATION:

APPLICANT: The Scripps Research Institute

APPLICANT: Schultz, Peter G

APPLICANT: Schultz, Peter G

APPLICANT: Chin, Jason

APPLICANT: Liu, David R

APPLICANT: Meggers, Eric L

APPLICANT: Meggers, Eric L

APPLICANT: Mestinak, Miro

APPLICANT: Santoro, Stephen W

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; ORGANISM: Plasmid
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Pred. No. 4.3e-181;
0; Mismatches 17;
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Sequence 1, Application US/10819386A
Publication No. US20050089884A1
GENERAL INFORMATION:
APPLICANT: Korea advanced Institute of Science
APPLICANT: Shanghai Jiaotong University
APPLICANT: LEE, Sang Yup
APPLICANT: LEE, Sang Yup
APPLICANT: DENG, ZIXIN
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FILE REFERENCE: PO03-B015
CURRENT APPLICATION NUMBER: US/10/819,386A
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: KR10-2003-0074035
PRIOR APPLICATION NUMBER: KR10-2003-0074035
NUMBER OF SEQ ID NOS: 28
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ZHOU, XIUFEN
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Pred. No. 5.1e-16;
0; Mismatches 497;
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; ORGANISM: Streptomyces noursei ATCC 11455
US-10-203-295-35
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APPLICANT: Brautaset, Trygve
APPLICANT: Strom, Arne Reidar
APPLICANT: Strom, Arne Reidar
APPLICANT: Valla, Svein
APPLICANT: Ellingsen, Trond Erling
APPLICANT: Sletta, Havard
APPLICANT: Gulliksen, Ole-Martin
TITLE OF INVENTION: Movel genes encoding a nystatin pol
TITLE OF INVENTION: manipulation and utility
FILE REFERENCE: 1181-265
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CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/GB 01/00509
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR FILING DATE: 2000-02-08
PRIOR PELICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0009387.2
PRIOR APPLICATION NUMBER: GB 0009387.2
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Best Local Similarity
Matches 455; Conserv
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Publication No.
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APPLICANT: Sekurova, Olga Nikalayivn
APPLICANT: Fjaervik, Epsen
APPLICANT: Brautaset, Trygve
APPLICANT: Strom, Arne Reidar
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SOFTWARE: PatentIn version
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                                            CGCACGCCGCGGGCTGCTCGCCGCGCACCTGGCCGCGC---CGGGCACCGAGGCCGAGA
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TCGCGGCCCACGCCCCCGGCGTCCAGCACGTGGGCCTCAACCCGATGTTCGCCCCCGCCG
                                                                                         TGCGGCCGGGCGCTGCTCGCCGACACCCTGTCCGTCCGGACGGGCATGGCCGCGGAGC 322
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Pred. No. 5.8e-16;
0; Mismatches 459;
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APPLICANT: Seturova, Olga Nikalayivna
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Statutaset, Tryyye
APPLICANT: Strom, Arne Reidar
APPLICANT: Strom, Arne Reidar
APPLICANT: Slingsen, Trond Erling
APPLICANT: Slilingsen, Trond Erling
APPLICANT: Gulliksen, Ole-Martin
ITILE OF INVENTION: manipulation and utility
FILE REFERENCE: 1181-265
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT APPLICATION NUMBER: US/10/203,295
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0009387.2
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
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FEATURE:
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US-10-156-761-7339
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NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7339
LENGTH: 4569
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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ISHIKAWA, JUN
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SHIBA, TADAYOSHI
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Pred. No. 3.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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SAKAKI, YOSHIYUKI
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HORIKAWA, HIROSHI
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                 Sequence 3440, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3440
LENGTH: 1884
TYPE: DNA
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APPLICANT: YANAI, KOji
APPLICANT: SUMIDA, Naomi
APPLICANT: WATANABE, Mana
APPLICANT: MORIYA, Tatsuk
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SEQ ID NO 5
LENGTH: 969
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Publication No. US20040214274A1
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CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: 82227/2001
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 40
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APPLICANT: MORIYA, Tatsuki
APPLICANT: MURAKAMI, Takeshi
TITLE OF INVENTION: Transformants Producing Substance PF1022 Derivatives, Methods
TITLE OF INVENTION: Producing The Same And Novel Biosynthesis Genes
FILE REFERENCE: 2003-1302A/WMC/00144
FILE REFERENCE: 2003-1302A/WMC/00144
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APPLICANT: OMURA, SA'
APPLICANT: IKEDA, H,
APPLICANT: ISHIKAWA
APPLICANT: HORIKAWA
APPLICANT: SHIBA, T.
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, THADYOSHI
APPLICANT: SAIBA, THADYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
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Best Local Similarity
Matches 342; Conserv
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SEQ ID NO 4723
LENGTH: 1707
TYPE: DNA
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LOCATION: (1)..(1707)
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Pred. No. 1.3e-13;
0; Mismatches 365
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; FEATURE:
; AMME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t
US-10-156-761-1
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US-10-156-761-1
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                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                 Matches 342;
                                                                                Query Match
Best Local
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT PPLICATION UNMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
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PRIOR FILING DATE: 2001-08-02
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HORIKAWA, HIROSHI
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WS-10-126-927-68/c

| Sequence 68, Application US/10126927
| Sequence 68, Application US/10126927
| Publication No. US20030082575A1
| GENERAL INFORMATION:
| APPLICANT: The Scripps Research Institute
| APPLICANT: The Scripps Research Institute
| APPLICANT: Wang, Lei
| APPLICANT: Manderson, John C
| APPLICANT: Anderson, John C
| APPLICANT: Liu, David R
| APPLICANT: Medilery, Thomas
| APPLICANT: Medilery, Thomas
| APPLICANT: Medilery, Thomas
| APPLICANT: Pastrnak, Miro
| APPLICANT: Pastrnak, Miro
| APPLICANT: Santoro, Stephen W
| APPLICANT: Santoro, Stephen W
| APPLICANT: Pastrnak, Miro
| APPLICANT: Pastrnak, Miro
| APPLICANT: Pang, Zhiwen
| TITLE OF INVENTION: In Vivo Incorporation of Unnatural
| FILE REFERENCE: 54-000120US
| CURRENT FILING DATE: 2002-04-19
| PRIOR APPLICATION NUMBER: US 60/285,030
| PRIOR APPLICATION NUMBER: US 60/355,514
| PRIOR FILING DATE: 2002-02-06
| NUMBER OF SEQ ID NOS: 79
| SOOFTWARE: Patentin version 3.1
| SEQ ID NO 68

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RESULT 14
US-10-126-927-67/c
US-10-126-927-67/c
; Sequence 67, Application US/10126927
; Publication No. US20030082575A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Schultz, Peter G
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; ORGANISM: Streptomyces
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Pred. No. 1.6e-13;
0; Mismatches 413;
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APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
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SEQ ID NO 67
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO:
APPLICANT: SHIBA, TADAYOSI
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SEQ ID NO 6049
LENGTH: 1167
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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Search completed: October 5, 2005, 09:57:35
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ALIGNMENTS

VERSION KEYWORDS SOURCE ORGANISM JOURNAL REFERENCE REFERENCE AUTHORS TITLE FEATURES COMMENT ACCESSION DEFINITION AUTHORS TITLE JOURNAL source Submitted (17-NOV-2003) Masahira Hattori The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Yu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abc@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9199, fax: 81-298-36-9199 sequence. AG441877 AG441877.1 GSS. R.Site 1 R.Site 2 Sequencing : TJ LIBRARY Hattori,M., Toyoda,A., Noguchi,H!, Kojima,T. and Sakaki,Y. BAC end Sequences of Library MSMg01 Unpublished Mus musculus molossinus Mus musculus molossinus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Vector e-mail: abe@rtc.riken.jp 2 (bases 1 to 1462) Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submission Mus musculus molossinus PRIMERS AG441877 /organism="Mus musculus mol /mol_type="genomic DNA" /sub_specise="molossinus" /db_xref="taxon:57486" /clone="MSMg01-323H09.TJ" Location/Qualifiers /tissue_type="mixture of kidney and spleen' /clone_lib="MSMg01 Mouse Male BAC Library" : pBACe3.6 : EcoRI : EcoRI. sex="male" . . 1462 GI:48084940 1462 DNA, bp DNA linear (clone:MSMg01-323H09.TJ, molossinus" GSS 03-JUN-2004 genomic survey

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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                                                                           Conservative
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/mol type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-168A20.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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sences of Library MSMg01
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                                                                                                                                                                                                                                                                                                  Score 133; DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
University of Washington
Box 352145, Seattle, WA
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chris K. Raymond
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                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            craymond@u.washington
                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                            /clone="pacs2-164_8365"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164
                                                                                                                                                                                                                                                                                db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                              organism="Pseudomonas"
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/clone_lib="Ppa EcoR! BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoR! and cloning into the BAC
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/mol_type="genomic DNA"
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Hattori, M., Toyoda, A
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                               /sub_species="molossinus"
/db_xref="taxon:57486"
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              /clone="MSMg01-192D21
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Sushiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, C (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/Tel:81-45-503-911], Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riker Tsukuba Institude, Bio Resource Center, Tsukuba Institude of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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/mol type="genomic DNA"
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Matches Query Match

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                                                                                           tissue_type="mixture of kidney and spleen"/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 1.1e-11;
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Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetes incertae sedis; Magnaporthace;
1 (bases 1 to 1137)
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Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 919-513-0024
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                                                                                         GACGGGCATGGCCGCGGAGCTCGCGGCCCACGCCCCGGCGTCCAGCACGTGGGCCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface"
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/mol_type="mRNA"
/strain="70-15"
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/clone="mgct002xd01f"
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0; Mismatches 468;
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AGENCOURT_6393396 NIH_MGC_72
5', mRNA sequence.
BM450237
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1 (Dases 1 to 1350)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: LLAM12204 row: p column:
                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                 quality sequence stop: 370.
/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clome="MRAGE:5528315"
/tissue_type="melanotic melanoma"
/tlab host="pH108 (phage-resistant)"
/clome_lib="NIH MGC_72"
/clome_lib="NIH MGC_72"
/clome_lib="NIH MGC_72"
/clome_skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Site_2: SalI; Cloned unidirectionally.
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Mus musculus molossinus
Mus musculus molossinus
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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/clone_lib="MSMg01 Mouse Male BAC Library"
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1 (bases 1 to 1198)

Kremitzki,C., Higginbotham,J., Wýlie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                              Insert Length: 182000 Std Error: 0
Seg primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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/mol type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-138F22"
/sex="female"
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/clone lib="CH261"
/clone lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: Eco
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
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R.Site 2
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, J
(B-mail:hattori@geo.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
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phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                             Conservative
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/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                      /clone="MSMg01-217C03.TJ"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/clone_lib="MSMg01 Mouse
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1073)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, I.
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
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Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the region [20,195].
Plate: L5B017 row: G
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Bioinformatics
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/db_xref="taxon:4565"
/clone_lib="Triticum_aestivum_FGAS: Library_5 GATE
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0; Mismatches 427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
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Class: BAC ends
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CL090560.1 GI:40584195
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Contact: Richard K Wilson
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Mardis,E. and Wilson,R.
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                                                                                                                                                                                                                                             /organism="Xenopus tropicalis"
/mol type="genomic DNA"
/db_xref="taxon:8364"
/clone="ISB1-17N15"
/clone_lib="ISB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus tropicalis"
/mal_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="CH216-160I16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Ballen. sessions@syngenta.com
Bmail: allen. sessions@syngenta.com
ABRC Stock Number CS812057; T-DNA left border flanking sequences
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Pat Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAIL_258_B06.v1,
SAIL_258_B06.v1,
CL476590
                                                                                                                                                                                                                                                        Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
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1 (bases 1 to 1267)
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/clone="SAIL 258_B06.v1"
/clone=1b="SAIL Collection"
/note="T-DNA left border sequences
modified TAIL-PCR strategy"
                                                                                           db_xref="taxon:3702"
                                                                                                                   /mol_type="genomic
/ecotype="Columbia"
                                                                                                                                                               organism="Arabidopsis thaliana"
                                                                                                                                                                                                          ocation/Qualifiers
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R.Site 1
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Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus molossinus
Mus musculus molossinus
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing : TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Toyoda,A., Noguch
BAC end Sequences of Library
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/db_xref="taxon:57486"
/clone="MSMg01-165A22.TJ"
/sex="male"
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/clone_lib="MSMg01 Mouse Male BAC Library"
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GGGTTCGCCTTCGCCCCGCGTTCGGCGTTCGACGTCCGGGCCCTCGGCGGCACGGCACCGCCGCGCGCG	GGCTCGCCTCGCCCTCGGCGTCGACGTCGACGTCGGGCCCTGGGCGGCACGGCACCGCGCGCG	GGCTCGCCCTCGGCCTCGGCGTCGACGTCGACGTCCGGGCCCTCGGCGGCACGGCACGGCACCGCCGCGCTCGGCCTCGGCCGCTCGGCGCGCGC	GGCTCGCCCTCGCCCCCGCGCTCGACGTCGACGTCCGGGCCTGGCGGCACGGCACCGCCGCGCGCG	GGCTCGCCCTCGCCCCTCGGCGTCGACGTCCGGGCCCTGGCGGCGACGGCACCGCCGC	

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Search completed: October 5, 2005, 09:01:18 Job time: 3671.67 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool_h/US10089514/runat_04102005_105744_8033/app_query.fasta_1.1621
-Q=/cgn2 1/USPTO_spool_h/US10089514/runat_04102005_105744_8033/app_query.fasta_1.1621
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICON=200 -THR_SCONE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

RESULT 1
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DEFINITION
Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene.
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCES
ORGANISM
E178315.1 GI:30015580
WO 02077244-A/3.
SOURCES
Streptomyces venezuelae
ORGANISM
REFERENCE
AUTHORS
TITLE
Transformant producing PF1022 substance and process for producing the same and novel biosynthetic gene
JOURNAL
MEIJI SEIKA KAISHA LTD, KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE,
PR 22-MAR-2002 WO 2002JP002782
PR 22-MAR-2001 JP 01P 082227
PI KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE, TATSUKI MORIYA, NAOMI SUMIDA, MANABU WATANABE, TATSUKI MORIYA, NAOMI SUMIDA, MANABU WATANABE, PI KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE, PI KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE, PI KOJI YANAI, NAOMI SUMIDA, MANABU WATANABE, PI MURAKAMI
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                                         GlySerProGluValTyrGlyAspIleGlnArgSerAsnProArgAlaAlaSerAlaArg
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ArgAlaLeuAlaGluAlaLeuArgSerPheAlaAlaLeuValGlyAspAspProAspArg
                                                                                  AlaAlaThrAlaProProProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeuGly
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                                GGCAGCCCGAGGTGTACGGGGACATCCAGCGGTCCAACCCCCGGGCGGCGTCCGCGCGC
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Transformant producing PF1022
producing the same
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(1). (966).
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:54571"
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Streptomyces venezuelae
Streptomyces venezuelae
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Transformants that
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:54571"
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                                                                                                                                        AB116234 5251 bp DNA linear BCT 03-JUL-2004 Streptomyces venezuelae papA, papC, papB, ORFIV genes for 4-amino-4-deoxychorismate synthase, 4-amino-4-deoxyprephenate dehydrogenase, 4-amino-4-deoxychorismate mutase, hypothetical
                Streptomyces venezuelae
                                                                                          dehydrogenase, 4-aprotein, complete AB116234
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Streptomycineae; Streptomycetaceae; Streptomyces.
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The gene cluster for chloramphenicol biosynthesis in Streptomyo venezuelae ISP5230 includes novel shikimate pathway homologues a monomodular non-ribosomal peptide synthetase gene Microbiology 147 (Pt 10), 2817-2829 (2001)
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Streptomyces venezuelae chloramphenicol biosynthetic partial sequence.
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Streptomyces venezuelae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                St, Halifax, NS B3H 4J1, Canada
Sequence update by submitter
On Jun 5, 2001 this sequence version
Location/Qualifiers
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                                  chloramphenicol biosynthesis"
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1 MetSerGlyPheProArgSerValValGlyGlySerGlyAlaValGlyGlyMetPhe
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3576. . .3596

'ACMORTING OF COLLAPAGNER FRADTALTGTEP"
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reductase-like domains near C-terminus"
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Conservative:
Mismatches:
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Gaps:
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888 bp. Sequence 2 from Patent WO9601901. A48324 A48324.1 GI:2302117	5 AspaspGluGlyGluLysAspArg 322 	ProGluLeuAlaAlaGlyGlnAspHisCysG	GlyCysAspGlyAlaGlyAsnLeuAs	7AspProAspArgAlaAspAlaProd	1 ArgAlaLeuAlaGluAlaLeuArgSerPheA 	1 GlySerProGluValTyrGlyAspIleGlnÁr: 	AlaAlaThrAlaProProProHisGlnVal	1 AlaValLeuLeuSerPheGlyLeuAlaLeuÁla :::	ValArgLeuThrAlaGluGluHisAspArg' 	ArgAspGlyProGlyValThrAl	1 ASNPROMETPHEAlaPROAlaAlaGlyMetThrGlyArg	ArgThrGlyMetAlaAlaGluLeuAlaAl 	1 ValAlaProValThrArgLeuMetArgProGlyAlaLeuLeuAlaAspThrLeuSerVa 	AlaLeuArgAspAlaAspLeuVal GCCTCCGGGACGCGGACCTCGTC	1 GlyArgProAspAlaCysLeuValGlyAspValThrAlaP 	1 AlaGlyLeuLeuArgGluAlaGlySerArgThrLeuVa 	ATGAGO
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linear		eArgThrLeuHis CCGCACCCTCCAC	LeuArgA ACTCCGCC	PAlaProGly	GlyAsp GCGAC	coArgAlaAl ccegeceec	LeuA.	LeuGlyValAspValArgA 	ThrGln BACCCAG	uGlyGlyG GGCGGCG	ProValAlaAlaVal CCCGTGGCCGCCGTG	yValGlnH CGTCCAGC	wAlaAspT CGCCGACA	uAspValAl GGACGTGGC	ProGlyProG 	alValAspLeuValPr CGTCGACCTCGTACC	AGCGGTGG
PAT			rgLeuM 3GCTCA	LYH18	ACCCG	aSe 	laArgVali cccgTgTgc	alArg	laLeu CCCTG	ద్దెద్ద	laval cccrc	isVal	CCCTC	laLeuLy cccrcaa	luLev AGCTC	alpro TACCG	GCGGC
07-MAR-		ArgThr GCACC	MetGly ATGGGA	ProGly	GACCCGGACCGC	cAlaArg GCGCGC	LeuGly CTCGGC	AlaLeu GCCCTG	AlaLeuThrHis CCCTGACGCAC	lyArgPro cAGGCCC	alvalThr regreace	GlyLeu GGCCTC	SerVal	Lysala AAGGCC	roGluLeuAlaAla CCGAGCTCGCGGCC	ProPro	ATGTTC
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1 (bases 1 to 888)

8 Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F.,
Barriere, J., Debussche, L., Famechon, A., Paris, J. and
Dutruc-Rosset, G.

STREPTOGRAMINES AND METHOD FOR PREPARING SAME BY MUT
Patent: WO 9601901-A 2 25-JAN-1999;
RHONE POULENC RORER SA (FR)
Other publication AU 2891295 960209
Other publication FR 2722210 960112.

Location/Qualifiers
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Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
             LeuAlaAlaThrAlaProProProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeu
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                                                                                                                                                                                                                         LeuAsnProMetPheAlaProAlaAlaGlyMetThrGlyArgProValAlaAlaValVal
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Blanc, V., Thibaut, D., Bamas-Jacques, N., Blanche, F., Crouzet, J.,
Barriere, J.-C., Debussche, L., Famechon, A., Paris, J.-M. and
Dutruc-Rosset, G.
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Other publication AU 2891295 960209
Other publication FR 2722210 960112.
Location/Qualifiers
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Blanc, V., Thibaut, D., Bamas-Jacques, N.,
Barriere, J., Debussche, L., Famechon, A.,
Dutruc-Rosset, G.
                                                                                                                                                                                                                                                                                                                                                              Sequence
A48323
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Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinobacteria; Streptomyces.
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                                                        /organism="Streptomyces pristinaespiralis"
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                            CTGGAACGCCTGTGCGCGCGCGATGTTCACCGCCCTGCAC
                                                      GlyGlnAspHisCysGlnGluLeuPheArgThrLeuHis
                                                                                                          GlyAsnLeuAspGlyValPheGlyGluLeuArgArgLeuMetGlyProGluLeuAlaAla
                                                                                                                                                                                                                                     ArgArgAlaLeuAlaGluAlaLeuArgSerPheAlaAlaLeuValGlyAspAspProAsp
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Dutruc-Rosset, G.
Streptogramins for preparing same by
Patent: US 6352899-A 1 05-MAR-2002;
Location/Qualifiers
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Blanc, V., Thibaut, D., Bamas-Jacques, N.,
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                                                               HisAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAla
                                                                                                                                                    GTCACCGACGGGCCCGGTGTGCGGGGCCCCTGGTGGAGCTGGTGGCCGGGTGGGGGCCCCGG
                                                                                                                                                                      ThrArgAspGlyProGlyValThrAlaLeuLeuArgLeuValGluGlyGlyGlyGlyArg
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                                          CATGCCGCGGTGCTGGGCCTGGGCCTGGGTGAGCTGTGGGACGTGGGGGGCG
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/mol_type="unassigned
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1 (bases 1 to 4740)
Blanc, V., Gil, P., Bamas-Jacques, N., Lo
Schleuniger, J., Bisch, D., Blanche, F.,
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Blanc, V., Gil, P., Bamas-Jacques, N.,
Bisch, D., Blanche, F., Debussche, L.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pristinaespiralis encoding enzymes involved in the biosynthesinthe 4-dimethylamino-L-phenylalanine precursor of pristinamycin Mol. Microbiol. 23 (2), 191-202 (1997)
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Streptomyces pristinaespiralis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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4740 bp DNA linear BCT 07-MAR-: Streptomyces pristinaespiralis 4-dimethylamino-L-phenylalanine precursor biosynthesis (papA, papC, papB, papM) genes, complete
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                             /organism="Streptomyces
/mol_type="genomic DNA"
/db_xref="taxon:38300"
68._.2227
APAPPASAPVGEYRLHVREVACVPDADAAFTALFADAPARFWLDSSRVEPGLARFTFL
GAPAGPLGEQITYDVADRAVRVKDGSGGETRRPGTLFDHLEHELAARALPATGLPFEF
                                                                                                                                                                                                                           /gene="papA"
68. .2227
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                                                                                                                                    product="PapA"
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quai Jules Guesde, B. P.
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.., Crouzet,J.
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Seine cedex 94403
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                SerGlyPheProArgSerValValValGlyGlySerGlyAlaValGlyGlyMetPheAla
      ArgProAspAlaCysLeuVal-----GlyAspValThrAlaProGlyProGluLeuAla
                                                                                                                                 GlyLeuLeuArgGluAlaGlySerArgThrLeuValValAspLeuValProProProGly
                                                                                                                                                                                                                      (1-322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transT_table=11
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/protein_id="AAC44869.1"
/db_xref="GI:1575339"
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EDEWILAGGGAPVTPVHASASARGAVS"
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/protein_id="AAC44867.1"
/protein_id="AAC44867.1"
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GARVVEMPARRHDELTAAQQAATHAAVLAFGLGGGELSVDVGALRDSAFPFHLAMLAL
LARIAGGTFEYYFDIQAANFGAPAARQALGRGLVRLGQAVERGDEETFAALFAELRGV
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ATAPAAERWLTDAARTLATTAPRPPFTILLPDDQLPALDVHYRHSLPRYRELVEECRRL
ITDGETYEVCLTNMLRVPGRI DPLTAYRALRTVSPAPYAAYLOFPGATVLSSSPERFL
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DIGSVHYPGLEFVETYATVHQLVSTVRGRLAADVSRPBAVRAAFPGGSMTGAPKVRTM
QFIDRLEKGPRGVYSGALGYFALSGAADLSIVIRTIVATEEAATIGVGGAVVALSDPD
DEVREMLLKAQTTLAALRQAHAGATASDRELLAGSLR"
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RRNARGTGARIVQGDARDAFPELSGTVDLVVTNPPYIPIGLRTSAPEVLEHDPPLALM
AGEBGLGMIRAMERTAARLLAPGGVLLLEHGSYQLASVPALFRATGRWSHASSRPTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="papM"
3799. .4677
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3413. .3802
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/gene="papC"
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/function="N-methylase"
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/function="mutase"
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                                                                                                             complete genome.

Complete genome.

Photorhabdus luminescens subsp. laumondii TTO1

Photorhabdus luminescens subsp. laumondii TTO1

Bacteria; Proteobacteria; Gammaproteobacteria;

Enterobacteriaceae; Photorhabdus.
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Duchaud, E., Rusniok, C., Frangeul, L., Buchrieser, C., Taourit, S., Bocs, S., Boursaux-Eude, C., Chandler, M., Dassa, E., Derose, R., Derzelle, S., Freyssinet, G., Gaudriault, S., Givaudan, A., Glaser, P. Medigue, C., Lanois, A., Powell, K., Siguier, P., Wingate, V., Zouine, M., Boemare, N., Danchin, A. and Kunst, F.
                                                                                                                                                                                                                                 segment 13/17.
BX571871 BX470251
BX571871.1 GI:36786846
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RBS
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of the entomapathogenic bacterium Photorhabdus luminescens Nat. Biotechnol. 11 (1) (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1142. .3028)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:243265"
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CDS

RBS

gene

RBS

CDS

gene

RBS

gene CDS

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Similar to

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29787

29727

29550

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                    AGTGGGGCAAAGGCGGTCGTCTTTGCCTTACCGGAAGCCGTCGCCATACAAGCGTTGCCT 30087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCATCCTTGGTGGGCAAGGCGCTATTGGTTCTTTATTAGAGCGCCTTTTTACTCAATAT 30264
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                                                                                                                                                                                                                                                                                          TCTCATTACTGTCAGATT---GATATCTTAAACCCGGCTGCTGATGTTGGAGCGGTTTTG 30147
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382.00
47.94%
32.06%
23.36%
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
50
126
38
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
AX770909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
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REFERENCE	JOURNAL MEDLINE PUBMED	TITLE				REFERENCE AUTHORS	ORGANISM	VERSION KEYWORDS SOURCE	ACCESSION	AE011181 LOCUS		P &	g &		Ş	g Qy		Qy b		DЬ	8				\$ 5		DЬ
2 (bases 1 to 12180)	Physiological D Genome Res. 12 21929760 11932238	Macario, A.J.L., Paulsen, I., Pritchett, M., Sowers, K.R., Swanson, R.V., Zinder, S.H., Lander, E., Metcalf, W.W. and Birren, B. The Genome of M. acetivorans Reveals Extensive Metabolic and	<pre>Krzycki,J.A., Leigh,J.A., Li,W., Liu,J., Mukhopadhyay,B., Reeve,J.N., Smith,K., Springer,T.A., Umayam,L.A., White,O., White,R.H. de Macario, E.C. Forry, J.G. Jarroll K.F. Ting H</pre>	Zimmer, A., Barber, R.D., Cann, I., Graham, D.E., Grahame, D.A., Guss, A., Hedderich, R., Ingram-Smith, C., Kuettner, C.H.,	- B R	zzi,M.G., Macdona			<pre>Methanosarcina acetivorans str. C2A, section 526 of 534 complete genome. AE011181 AE010299</pre>	AE011181 12180 bp DNA linea	TO THE CONTRACT CONTRACT CONTRACT CONTRACT CANDIDATES AND A CONTRACT CONTRA	236 aAlaSerAlaArgArgAlaLeuAlaGluAlaLeuArgSerPhe 250	216 AAFGVALLeuGIYGIYSEPPROGIUVALTYRGIYASPILEGINARGSEFASNPROARGAI 236 ::: :::	6987 CATCGAAGAGGTCGCCAGCCCCGTGTATCGCCTACTCATGGACGTCGTGGG 7037	hrAlaPr	180 sAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAs 196		6807 GCGTAGTGGTCCCTGGACTCGCCGCGTTCGTCGTTATCTCGAGCGGAAAAGGCGCTCGAGT 6866 160 oValArqLeuThrAlaGluGluHisAspArqThrThrAlaAlaThrGlnAlaLeuThrHi 180	-ArgAspGlyProGlyValThrAlaLeuLeuArgLeuValGluGlyGlyGlyGlyArgPr	TTCGGCCCACGGTCCCCAGTCTCCGCGGT	122 oMetPheAlaProAlaAlaGlyMetThrGlyArgProValAlaAlaValValThr 140		yMetAlaAlaGluLeuAlaAlaHisAlaProGlyValGlnHisValGlyLeuAsnPr	GGTCGCACCACACGTTCCTGAGGGTTCCCTCTCACCGACGTGACCTCCGTCAAGGTTCG		63 gAspAlaAspLeuValLeuLeuAlaValHisGluAspValAlaLeuLysAlaValAlaPr 83	:::
gene				CDS	gene				CDS	gene												CDS	gene		source	1	AUTHORS TITLE
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Matches:
Conservative:
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Indels:
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                                                                                 ORGANISM
    AUTHORS
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                   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinaceae; Methanosarcina.

1 (bases 1 to 9888)
                                                                               Methanosarcina
Methanosarcina
                                                                                                                                              complete genome.
AE013358 AE008384
AE013358.1 GI:20905730
                                                                                                                                                                                                          AE013358 9888
Methanosarcina mazei strain
Deppenmeier, U.,
                                                                                                                                                                                                                                                                                                                 AGCCTGGTA 11467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuValGluGlyGlyGlyArgProValArgLeuThrAlaGluGluHisAspArgThr 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGAACTTGACGCAGCCATCCCTGAAAACGATATAGTAATAGTATCCGTTCCGATCAAC 10918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGGAAAAACGAAGGTTTTGATCCTTGGCGGAACCGGAGAGATGGGGCAGTGGTTCACT 10768
                                                                                                                                                                                                                                                                                                                                                        AlaLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                 GAAAACCCGGGTATTCCGGAGGTGCATGAAGCATTTATAGAGGAATGTGAGGAACTTTCC 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGACTTTGTGGGCAGGATCCTGGGCCAGAACCCCTACCTCTACGCCCTGATCCAGATG 11398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTCGGTAGTACAGGGGCTGACGCATTTTGCTTATATCTCAATAGGGACGACCATTGAC 11278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGTAATCCTTGTCCCGGTAAAGGAGCGCTCGGAAAAATGGTTTCCCGGTAATCAGGCAG 11158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGAGATTCTCGGAACGCACCCCATGTTCGGGCCCACGATTCCCACCATCAGGGGACAA 11098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGlnHisValGlyLeuAsnProMetPheAlaProAla---AlaGlyMetThrGlyArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspThrLeuSerValArgThrGlyMetAlaAlaGluLeuAlaAlaHisAlaPro---Gly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGCCAGGAAACTGAATGTACCCTTTGCT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTTTTTTAAAGAAAGGGGTTATAAGGTTACGGTCTGGGGAAAAAGGGGGCAAGGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnProArgAlaAlaSerAlaArgArgAlaLeuAlaGluAlaLeuArgSerPheAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAlaLeuLeuAlaArgValLeuGlyGlySerProGluValTyrGlyAspIleGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCTTGATTTCGACATCAAGAAATCCAGGAAATTCGTAAGTCCGGTCTACAGTATAATG 11338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgLeuGlyValAspValArgAlaLeuAlaAlaThrAlaProProProHisGlnValLeu 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTTTGAGGAAGGCGGAGCCCACGTTGAAÁTCACGACCGCAGCCGAACACGACAGGCTG 11218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTTTACCTCCACCAAGGTAAAGCCTGTTGAAGCCATGCAGAGGTTTGCACCTGCCGGG
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                                                                               mazei Gol
Johann, A.,
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rain Goel,
  Hartsch, T.,
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section
    Merkl, R.,
                                                                Methanosarcinales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez-Arias,R., Henne,A., Wiezer,A., Baeumer,S., Jacobi,C., Brueggemann,H., Lienard,T., Christmann,A., Boemecke,M., Steckel,S., Bhattacharyya,A., Lykidis,A., Overbeek,R., Klenk,H.-P., Gunsalus,R.P., Fritz,H.-J. and Gottschalk,G.
The genome of Methanosarcina mazei: evidence for lateral gene transfer between bacteria and archaea transfer between bacteria and archaea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGAHVEITTAEEHDRLVSVVQGLTHFAYIAIGTTIDRLDFDVKKSRKFVSPVYSIMLD
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5767. .7185
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4928. .5770
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Percent Similarity:
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GTCTCAGTAGTGCAGGGGCTTACTCATTTTGCTTATATTTGCTATAGGCACAACCATTGAC 635
                                                                                                                                                                                                                                                     ProValAlaAlaValValThrArg-----AspGlyProGlyValThrAlaLeuLeuArg 151
                                                                                                                                                                                                                                                                                                                                                                ValGlnHisValGlyLeuAsnProMetPheAlaProAla---AlaGlyMetThrGlyArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                       GATTTTACCTCAATAAAGGTAGGACCTGTTGAAGCGATGAGAAAGTTTGCGCCCAAAGAT 6114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAACAGAAGAAACCATCGCAGAAATCGCCCCAAAAATGAAAGCTGGAAGCATTCTTATG 605
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                                                                                                                                                                                                         ACAGTAATCCTTGTTCCGGTAAAAGGGTATTCGGAAAAATGGTTTCCGGTAATCAGACAG 623
                                                                                                                                                                                                                                                                                                               GTTGAAATTCTTGGGACGCACCCCATGTTTGGTCCGACAATTCCCCACAATAAGGGGGCAA
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                                            ThrAlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAlaLeuAla 191
                                                                                                                              LeuValGluGlyGlyGlyArgProValArgLeuThrAlaGluGluHisAspArgThr 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspThrLeuSerValArgThrGlyMetAlaAlaGluLeuAlaAlaHisAlaPro---Gly 114
                                                                                                     CTTTTTGAGGAAAGCGGCGCGCACGTTGAGATCACAACTGCAGAGGAACACGACAGGCTG 629:
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IRTVSGLIRSYKERNRHDPFKNKYQLIKNDLPLYSLKPGRVFGLLNDAGFEEINIERM
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DVRVAATIALGNIGSPEAVNVLKKTYENQNMMMVRNGALIALGKTENQEAAEFFIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-FEB-2004) Department of Microbiology, University of Washington, University of Washington Genome Center, Seattle, WA 98195-7242, and the Genome Analysis Group, Oak Ridge National Laboratory, Oak Ridge, TN 37831-6164
This strain was formerly known as LL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 268122)
Leigh, J.A., Olson, M.V. and Larimer, F.W.
Direct Submission
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Methanococcus maripaludis S2
Archaea; Euryarchaeota; Methanococci;
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BX957223 BX950229
BX957223.1 GI:45047859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCTTGATTTTGACGTCAAAAAGTCCAGAAAATTCGTAAGCCCGGTTTACAGTATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 268122)
                                                              /transl table=11
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227. .1555
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                                                                                                                                                                                                                                                                                                                                                 gene="secY"
                                                                                                                                                                                                                                                                                                                                                                                                                     gene="secY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:267377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain="S2"
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udis S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LITLVGGAILVSLSTGLSGFINWILSPIGFTVINEATKITGWPNVYMTVSELAIPTVT
DIIENSVGNIWLLIAGISGILLSFVSERHDKOKIDIKKALYITHLIATVYAATKGEIFRIR
FVALMTPALAIGIGIFAGOIENIKRYEKVESFILVFVIGILSVITLIKYGGELFNIL
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TEAKASLVNNYDLTDAEAEEVLDITHFKVTNPDYLITYMRTSLASVWSMFGNWNFSL
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                                                                                                                                                                                                                                    order(2648. .2707,2999. .3067,3086. .3145,3173. .3232, 3257. .3310,3320. .3379,3413. .3481,3611. .3670,3704. 3767. .3865,3863. .3922,3950. .4018,4055. .4123) /locus tag="MMP1424" /note="13 probable transmembrane helices predicted by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Oligosaccharyl transferase, STT3 subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLAAAADFTGALGGGTGVLLTVSIVYRLYEQLVQEQLSELHPSIAKFIRK"
order(317. .385,443. .511,572. .640,650. .709,728. .796,
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5262. .5801
                                                                                                                                                                                               /note="13 probable transmembrane helices predicted by TMHMM2.0"
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SKNLEDSIYTKLHFLDGYGLEKISLEKESVDPTSYGIQPGFKVYSVDYGTDYLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYAPPGREAGLVSALSIATVLVYSVWNSIDSTVTIMNAAFWVPAIMSIFLGIPVFFIV
RRNTASNIGGLVGALLLISSPSLLYKTSAGFSDTPIFEILPLLFIVWMIMEAIHEQEN
SKKSGIFGGIAAILIGLYPWMWSGWWYAFDITAGFLVLYTAYEYLTKSKNLKNVITTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="7 probable transmembrane helices predicted by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(order(1613. .1678,1853. .1918,1964. .2020,
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WAIEAFFGILSILYTKYFGFNIF"
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dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1595. .24
/locus_tag="MMP1423"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus tag="MMP1422"
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TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2591. .2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2591.
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/note="Signal predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="MMP1424"
2591. .5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_tag="MMP1424"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="secY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                               .5801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2494)
                                                                                                                                                                                                                                                                                                                                                              .3754,
                                                                                                                                                      gene
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                                        CDS
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EMA I GMI NKKTTAVR I I PVPGKDVGDYVEYGGLLGTAP I MPVSEFSSEEL I ERGGR I P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKAGINMYAVKKMGEIVKETSEITKDAIGCAKIVVFCNAPEDNPFMAGAFHGPGEGDA
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EVGITLDKIAKEVGVDFIGGYSALVQKRATYBEKMLIRSIPKLMTKTDKKVCASYNVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="MMP1427" 6449. .7825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="UniProt/TrEMBL:O6LXC6"
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                                                                                                                                                          complement(8114. .8431)
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Search completed: October 5, 2005, 15:36:38 Job time : 5131.02 secs

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Abd08026 Pseudomon
   Adg91050 Hepatic
                                               Abz66810 Orthosomy
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4-amino-4-deoxyprephenic acid dehydrogenase; enzyme; papC; Metabolite; benzene; chorismic acid; p-aminophenylpyruvic acid, 4-amino-4-deoxyprephenic acid dehydrogenase coding sequence. Location/Qualifiers /product= "4-amino-4-deoxyprephenic acid dehydrogenase"

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as to produce a secondary metabolite. The secondary metabolite has a controlled by the para-position by a controlled functional group, thereby enabling the production of a secondary metabolite with a benzene ring skeleton substituted at the para-position by a nitrogen-containing group. The transformant organism of the present invention has been produced by transferring a gene participating in the biosynthesis pathway from chorismic acid into paninophenylpyruvic acid. The present sequence is the coding sequence for 4-amino-4-deoxyprephenic acid dehydrogenase (papC), from Streptomyces venezuelae. papC participates in the biosynthesis pathway from chorismic acid into p-aminophenylpyruvic acid, and so the papC gene can be used to produce the transformant of the present invention. The transformant can be used to produce metabolites for application in pharmaceuticals,
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Murakami
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y Match:
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The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacy tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the -tRNA with at least one unnatural amino acid in the translation system and the O-tRNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Aspl2TAG mutant of chloramphenicol acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is provided exogenously. The translation system is a cell and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orthogonal aminoacyl tRNA synthetase; unnatural amino acid; chloramphenicol acetyltransferase; dihydrofolate reductase; ds; plasmid; biosynthesis; p-aminophenylalanine; pAF; chorismate.
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                                               CGGGCGCTCGCCGAGGCCCTGCGCTCCTTCGCCGCGCTGATCGGCGACGACCGGACCGGACCGC
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Alignment
                                                                                                                                               trnA with at least one unnatural amino acid in the translation system and the O-thNA recognises at least one selector codon. A composition of the invention is useful for producing at least one protein comprising at least one unnatural amino acid. The protein is the Aspl2TAG mutant of chloramphenical acetyltransferase (CAT), the Tyr163TAG mutant of mouse dihydrofolate reductase (DHFR), or a Tyr163TAG mutant of mouse dihydrofolate reductase comprising CHOOH His6tag. The unnatural amino acid is provided exogenously. The translation system is a cell and the unnatural amino acid is biosynthesised by the cell. The present sequence represents a plasmid for use in the biosynthesis of p-aminophenylalanine (pAF) in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel composition comprising a translation system comprising an orthogonal tRNA (O-tRNA) and an orthogonal aminoacyl tRNA synthetase (O-RS), where the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS preferentially aminoacylates the O-RS p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New streptogramin B derivs. useful as antibiotics - produced by new mutants of Streptomyces having altered genes for streptogramin B biosynthesis.
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P-PSDB; AAW11582.
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SerGlyPheProArgSerValValValGlyGlySerGlyAlaValGlyGlyMetPheAla

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US-10-089-514-6 (1-322)

x AAT59269 (1-888)

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RESULT 6
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AC AAT592
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Streptogramin B; antibiotic; biosynthesis; pristinamycin; virginiamycin; DMPAPA precursor; 4-dimethylamino-L-phenylalanine; papA; papM; papB; papC; isomerisation; aromatisation; N-methyltransferase; ds.
Streptomyces
pristinaespiralis.
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/*tag= c
/product= "PapB"
2259. .2888
                                                                                                                                                             /product= "PapA"
/note= "C-terminal coding
open reading frame"
/note= "N-terminal coding region only,
open reading frame"
                                                                                                                                                complement (949. .1836)
                           /*tag= d
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873. .2262
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WO9601901-A1

25-JAN-1996

95WO-FR000889

94FR-00008478.

(RHON) RHONE POULENC RORER SA

Blanc V, Barriere ŗ, Thibaut D, I J, Debussche Bamas-Jacques e L, Famechon ÞΖ Blanche F, Crouzet J;
Paris J, Dutruc-Rosset <u>ი</u>

1996-097631/10. DB; AAW11582, AAW11583

New streptogramin B derivs. useful as antibiotics - produced by new mutants of Streptomyces having altered genes for streptogramin B

Example 1; Page 102-104; 146pp; French.

pristinamycin IA. The region between these two genes was sequenced and two open reading frames were identified. The first (papc) was on the complementary strand and decodes to an amino acid sequence with homology to the region of E.coli TyrA which has been implicated in aromatisation reactions. The PapC gene product is likely to be involved in a similar aromatisation of 4-deoxy 4-amino prephenate to give 4-amino penylpyruvate during DMPAPA synthesis. The second open reading frame (papB) could be decoded to give a product with homology to the region of TyrA which has chorismate mutase activity. The PapB gene product is likely to catalyse the isomerisation of 4-deoxy 4-amino chorismate to 4-deoxy 4-aminoprephenate. Disruption of the papB and papC genes can be used to produce strains of S.pristinaespiralis which are unable to produce the antibiotic pristinamycin I but which may be able to produce new, modified forms of it The papA and papM genes of S.pristinaespiralis are involved in the biosynthesis of 4-dimethylamino-L-phenylalanine (DMPAPA), a precursor for

Sequence 2888 BP; 390 A; 1319 Ç 897 ູດ 282 Η, 0 0 Other 밁 Ş В á 밁 á В Ş В Ś 밁 Ş 밁 Ś 밁

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Query Match:
DB:
               Best Local
                    Percent Similarity:
                                     No.:
               Similarity:
             4.27e-30
661.50
60.38%
49.52%
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             Matches:
Conservative:
Mismatches:
       Indels:
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Photorhabdus luminescens nucleotide sequence #10241

detection; food; gene expression; plant; animal; microorganism; antibiotic; biopesticide; virulence factor; disease model; plag whooping cough; gene; ds. Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

Photorhabdus luminescens

WO200294867-A2

28-NOV-2002

07-FEB-2002; 2002WO-IB003040

07-FEB-2001; 2001FR-00001659

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Buchrieser Duchaud ᅜ Taourit S, Glaser P, Frangeul ŗ Kunst Ή, Danchin

O sequence of Photorhabdus luminescense.g. as therapeutic antimicrobials and and and and encoded polypeptides, agricultural pesticides.

Claim 2; SEQ ID NO 10241; 1205pp; French

The invention relates to the isolation of genes and their encoded CC proteins from Photorhabdus luminescens. The isolated sequences are consures of probes and primers for detecting the genome of P. luminescens CC and related species; to study polymorphisms; for gene analysis and for CC detection/amplification of the genes. Antibodies (Ab) raised against the CC polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC carry a gene-containing vector are used to select compounds that CC modulate, regulate, induce or inhibit expression of the genes in plants, and animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antiblotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC recombinant production of the proteins, particularly toxins and cells that CC genes, proteins, vectors containing the genes and Ab are also useful CC antibacterials useful as insecticides, bactericides and fungicides. The CC genes, proteins, vectors containing the genes and Ab are also useful CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence CC factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This cC sequence represents one of the isolated P. luminescens genes

BP; 207 A; 194 ü 229 G; 258 ij, 0 U; 0 Other;

á 밁 Š. Percent Similarity:
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Query Match: US-10-089-514-6 (1-322) x ACF71774 (1-888) Score: 28 19 œ GlySerArgThrLeuValValAspLeuValProProProGlyArg--ValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAla GTCATCCTTGGTGGGCAAGGCGCTATTGGTTCTTTATTAGAGCGCCCTTTTTACTCAATAT 3.92e-14 382.00 47.94% 32.06% 23.36% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 888 101 50 126 38

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P Sequence split into 7 f
P Fragment Name
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P ACF65387 2
P ACF65387 2
P ACF65387 3
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      LeuAlaAlaGlyGlnAspHisCysGlnGluLeuPheArgThrLeu
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                                                     TCCCGTTCGCGCTATGCTCGAGCACGCTCCCGAGGATGTGTACGTCCTCGGAACTCACCC
 TGACGAAGCCCGTGAAGAGCTCCTCCGCGCCCTCAGACGCTTC
                         aAlaSerAlaArgArgAlaLeuAlaGluAlaLeuArgSerPhe
                                                                                                           CATCGAAGAGGTCGCCAGC-----
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                                                                                                                                     pValArgAlaLeuAlaAlaThrAlaProProProHisGlnValLeuLeuAlaLeuLeuAl
                                                                                                                                                                  TGCTGTCCTCCTCGCTGCAGGCGCCCCCATAGGCCGTTTCCTCCCAAGTCTCGAGCTCGA
                                                                                                                                                                                            sAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArg-----LeuGlyValAs
                                                                                                                                                                                                                      CGTTGAGACCACCCCGGAGGAACACGATCGCACTATGGCCGTCGTTCAGTGCCTCACCCA
                                                                                                                                                                                                                                                                           GCGTAGTGGTCCCTGGACTCGCCGCGTTCGTCGTTATCTCGAGCGGAAAGGCGCTCGAGT
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Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:

237.00 45.39% 27.66% 14.50% 8

No.:

1.66e-05

Length:
Matches:
Conservative:

78 50 110 44 8

Sequence 1122 BP; 248 A; 242 C;

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<u>ი</u> 293 ., 0

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US-10-089-514-6

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Gaps: Mismatches: Indels:

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RESULT 11
AAD50753
ID AAD50
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                                                                                                                        Escherichia coli bifunctional prephenate dehydrogenase. Sequences of t invention are useful for producing a plant such as cannla, maize, Arabidopsis, Brassica campestris, B.napus, soybean, crambe, mustard, castor bean, peanut, sesame, cottonseed, linseed, safflower, oil palm, flax and sunflower having increased tocopherol levels, especially alph or gamma-tocopherol or tocotrienol relative to a plant with a similar genetic background but lacking the exogenous nucleic acid molecule. The are useful for reducing tocopherol levels in a plant. They are also useful for producing plant expressing homogentesic acid and plants of the development of the development and plant of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention comprise a promoter region functioning in a plant cell to cause production of an mRNA molecule linked to a heterologous nucleic acid molecule encoding an enzyme with prephenate dehydrogenase (tyrA) or chorismate mutase activities or a tyrA from Erwinia herbicola or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule encoding enzymes involved in tocopherol biosynthesis useful for enhancing or altering tocopherol production plants such as canola, maize, soybean, crambe, mustard, castor bean, peanut, sesame, or cottonseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel nucleic acid molecules encoding enzymes involved in tocopherol biosynthesis. Polynucleotides of the
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  264 ProGlyArgAlaAspAlaProGlyHisProGlyGlyCysAspGlyAlaGly----
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                           ATAAATCAGTGTAAGGAAATCAGTGAAATTGTTAAAAATAAAGATAGAGAAGGTTTTGTT
                                                                             GluValTyrGlyAspIleGlnArgSerAsnProArgAlaAlaSerAlaArgArgAlaLeu
                                                                                                                             GCCTCCCCAATATACGAGTTGATGATTTCTATCATTGGGAGGATTATAGGACAGAATCCC
                                                                                                                                                  AlaProProProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeuGlyGlySerPro
                                                                                                                                                                                                 LeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAlaLeuAlaAlaThr
                                                                                                                                                                                                                              GAGTGGTTTAACAAGGTTTATAATTTTTTAAAGAAAGAAGGGGCTAAGGTTATAGTCATC
                                                                                                                                                                                                                                                                                                    ProGlyValThrAlaLeuLeuArgLeuValGluGlyGlyGlyGlyArgProValArgLeu
                                                                                                                                                                                                                                                                                                                                                     AlaGlyMetThrGlyArgProValAlaAlaValValThr------ArgAspGly
                                                                                                                                                                                                                                                                                                                                                                                   AlaAlaHisAla---ProGlyValGlnHisValGlyLeuAsnProMetPheAlaProAla
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                                                  AlaGluAlaLeuArgSerPheAlaAlaLeuValGlyAspAspProAspArgAlaAspAla
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                                                                                                                                                Alignment
                                                                                                                                                                                                      The present invention relates to arogenate dehydrogenase (ADH) enzymes (see ABN83439-ABN83443 and ABB83248-ABB83251). The ADH enzymes catalyse the last stage of the metabolic pathway of tyrosine biosynthesis and are potential targets of herbicides. The present sequence is the coding sequence for prephenate dehydrogenase, which was used to illustrate the
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                          New nucleic acid herbicides, also
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-2000;
                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                  Disclosure;
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GTTATCGTCGGCGGTGGCGGTCAGATGGGACGCCTGTTCGAGAAGATGCTGACCCTCTCG
                ValValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAla
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       Shikimate pathway; chorismate mutage; tyrA; prephenate dehydrogenase; vitamin B; vitamin K; ubiquinone; fat-soluble antioxidant; transgenic; feed; pharmaceutical; cosmetic; aromatic amino acid; salicylic acid; folic acid; phenylpropanoid; flavanoid; plant; abiotic stress resistance; tocopherol; tocotrienol; gene; ds.
                                             Shikimate pathway; vitamin E; vitamin
                                                                                 E. coli tyrA
                                                                                                                                                         ABA99612
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                                                                                                                                                                                                                                                                                                           This invention describes a novel method for the preparation of fine chemicals by culturing organisms in which the shikimate pathway has been altered relative to the wild type. The method involves a construct containing a plastid transit peptide, a chorismate mutase and/or prephenate dehydrogenase, linked to at least one regulatory sequence for transcription or translation in plants. The method is used to produce chemicals, particularly Vitamins E or K and/or ubiquinone, useful e.g. as fat-soluble antioxidants (in feeds, pharmaceuticals and cosmetics), but also aromatic amino acids, salicylic or folic acid derivatives, but plants with increased Vitamin E contents have improved resistance to plants with increased Vitamin E contents have improved resistance to abiotic stress, e.g. frost and drought. Transgenic plants with an altered shikimate pathway are useful as foods, fodder and in preparation of processed foodstuffs. Transgenic plants with modified shikimate pathways and increased content of desired chemicals, particularly tocopherols and/or tocotrienols. This sequence encodes the Escherichia coli tyra (chorismate mutase prephenate dehydrogenase) protein used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing fine chemicals, particularly Vitamins E and K, useful as antioxidants e.g. in foods or medicine, by growing organisms with altered
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21-DEC-2000; 2000DE-01064454.
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Search completed: October 5, 2005, 10:51:48
Job time: 728.456 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
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-DB=Issued_Patents_NA -QFMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPPEXT=0.5 -DELOP=6 -DELEXT=7
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6 4 US-09-692-570-1
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1 4 US-09-557-884-1
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1 4 US-09-543-681A-1138
4 US-09-943-681A-1138
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ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                      ; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-2
                                                               Score:
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APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins and Method
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
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APPLICANT: THIBAL
APPLICANT: BAMAS-
APPLICANT: BLANCH
APPLICANT: COUZET
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DEBUSSCHE, Laurent
FAMECHON, Alain
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COUZET, Joel
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RESULT 2
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Sequence 2, Application U
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CURRENT APPLICATION NUMBER: US/09/987,614A
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/08/765,907
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 888
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ORGANISM: Streptomyces
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DUTRUC-ROSSET, Gilles
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DEBUSSCHE, Laurent
FAMECHON, Alain
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COUZET, Joel
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APPLICANT: FAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRIC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
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US-08-765-907A-1/c
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SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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DEBUSSCHE, Laurent
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APPLICANT: THIBAU
APPLICANT: BAMAS-
APPLICANT: BLANCH:
APPLICANT: COUZET
APPLICANT: BARRIE
                                                                                                                                                                                                                                                                                Sequence 1, Application US/09987614A Patent No. 6833382
                                                                                                                                                                                                                                                                   GENERAL INFORMATION
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/09/987,
CURRENT FILING DATE: 2001-11-15
                                                   APPLICANT: DEBUSSCHE, Laurent
APPLICANT: FAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method
TITLE OF INVENTION: Mutasynthesis
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                                                                                     BARRIERE, Jean-Claude
DEBUSSCHE, Laurent
FAMECHON, Alain
PARIS, Jean-Marc
DUTRUC-ROSSET, Gilles
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COUZET, Joel
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BAMAS-JACQUES, Nathalie
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Best Local Similarity:
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PRIOR FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
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RESULT 5
US-08-916-421B-1/c
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TITLE OF INVENTION:
FILE REFERENCE: PB275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bult et a TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22
                                                                                                                                   NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
OTHER_INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals
NAME/KBY: misc_feature
LOCATION: (84773)...(84773)
                                                  LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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                                                                                                         NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
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LOCATION: (98266)..(98266)
                                                                                                                                                                                                                      LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
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LOCATION: (84808)..
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                                                                                  NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
                                                                                                NAME/KEY: misc feature LOCATION: (741684). (741684) or the representation: n equals a, NAME/KEY: misc feature LOCATION: (779455). (779455) OTHER INFORMATION: n equals a.
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LOCATION: (234814). (234814)
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LOCATION: (855539)..(855539)
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LOCATION: (559167)..(559167)
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LOCATION: (309398)...(309398)
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Best Local Similarity:
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LOCATION: (1607912)..(1602912)
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LOCATION: (1603734)..(1603734)
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LOCATION: (1349473)..(1349473)
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TITLE OF INVENTION: Complete Genome
Patent No. 679746
TITLE OF INVENTION: jannaschii
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                                                                                                                                                               SEQ ID NO :
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PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF COO.
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CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20 SOFTWARE: PatentIn version
                                              NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals
                   NAME/KEY: misc_feature
                                                                                                    FEATURE:
                                                                                                               ORGANISM: Methanococcus
                                                                                                                                  TYPE: DNA
                                                                                                                                               LENGTH: 1664976
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FEATURE: MISC feature NAME/KEY: MISC feature
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LOCATION: (191389)...(191989)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals
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LOCATION: (234187)...(234187)
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LOCATION: (231980) . (231980)
OTHER INFORMATION: n equals
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LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals
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LOCATION: (163385)...(163385)
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LOCATION: (148948)..(148948)
OTHER_INFORMATION: n equals
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LOCATION: (103998)..(103998)
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LOCATION: (98266)..(98266)
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LOCATION: (98239)..(98239)
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LOCATION: (98159)..(98159)
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LOCATION: (98120)..(98120)
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LOCATION: (84812)..(84812)
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LOCATION: (84808)..(84808)
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LOCATION: (84773)..(84773)
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER_INFORMATION: n equals
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals
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LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals
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LOCATION: (657081)..(657081)
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LOCATION: (559167)..(559167)
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LOCATION: (871619)..(871619)
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LOCATION: (855539)..(855539)
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LOCATION: (682442)..(682442)
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LOCATION: (674435)..(674435)
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LOCATION: (657203)..(657203)
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LOCATION: (622708)..(622708)
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LOCATION: (559241)..(559241)
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LOCATION: (319226)..(319226)
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LOCATION: (312993)...(312993)
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LOCATION: (312837)...(312837)
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LOCATION: (309418)...(309418)
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RAME/KEY: misc_feature

NAME/KEY: misc_feature

1096846)..(1
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LOCATION: (1313224)..(;
OTHER INFORMATION: n e
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LOCATION: (1310988)...(1310988)
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LOCATION: (1119881)..(1119881)
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LOCATION: (1130881)..(1130881)
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 4572
LENGTH: 1131
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4572
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Sequence 4572, Application
Patent No. 6610836
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS A
FILE REFERENCE: 2709.2004001
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PATENT NO. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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445 GTTATCGTCAGCGTACCGATTCACACCACCGTGGAGAGCGATCGGCAGGCTGCCGCCCCTT
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                                                                                                                                                                COUNTRY: USA
ZIP: 20850
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                                                                                                                                                                                                                         CITY: Rockville
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Best Local Similarity:
Query Match:
DB:
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SEQUENCE CHARACTERISTICS:
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  1371285
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FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              140 ThrargaspGlyProGlyValThralaLeuLeuArgLeuValGluGlyGlyGlyArg
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                                     LeuAlaAlaThrAlaProProProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeu
                                                                                                                   HisAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAla
                                                                                                                                                                                                ProValArgLeuThrAlaGluGluHisAspArgThrThrAlaAlaThrGlnAlaLeuThr
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TYPE: nucleic acid
STRANDEDNESS: double
TTATTGGCACTTTCTTCCCCTATTTATCGGTTAGRACTTGCGATGATAGGTCGTTTATTT 1371344
                                                                               CATTTTTCGACTTTTGCGAATGGTTTACACCTTTCCAAACAGCCCATTAATCTCGCTAAT
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TELEFAX: 301-309-8439
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Matches:
Conservative:
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-643-990A-1
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US-10-089-514-6 (1-322)
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                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base
                                                                                                                                  No.:
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OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1995-04-21 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF
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                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Key West Avenue CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kenley K. Hoover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MD
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Owen White
Coven White
Hamilton O. Smith
J. Craig Venter
OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
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x US-09-643-990A-1 (1-1830121)
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                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1138
ENERGY SERVICES
                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-543-681A-1138
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                   Sequence 1138, Application Patent No. 6605709
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    Sequence 5637, Application U
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S
APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven
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SEQ ID NO 5637
LENGTH: 1038
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TITLE OF INVENTION: Myxococcus xanthus Genome FILE REFERENCE: 38-10(1.5849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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rAlaArgArgAlaLeuAlaGluAlaLeuArgSerPheAlaAlaLeuValGlyAspAspPr
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                                    ACGGCTGGAGGTGCCCCATCTCTTCGGCGTCGTGCAGTCGGAGAATCCCTACGCGCGGGA
                                                                  lLeuGlyGlySerProGluValTyrGlyAspIleGlnArgSerAsnProArgAlaAlaSe
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Section of the Steven C.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1269
LENGTH: 49225
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                                                                                                                                                                                                                                                                       84 ValThrArgLeuMetArgProGlyAlaLeuLeuAlaAspThrLeuSerValArgThrGly 103
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                                                                CTGTTCGGCCCGGCCAGTCT-GGCGAGGGGCGACCTGCCTCGCCGCACGGTGGTGTGCCC
                                                                                                     MetPheAlaProAlaAlaGlyMetThrGlyArgProValAla------AlaValVal 139
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                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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US-09-103-840A-1/c
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                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FLEISCHMAN, Robert APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                         LENGTH: 4411529
TYPE: DNA
                                          3936106
                                                                                                3936166 GCCGGTGCCGATCCCGCCGTCGCCGGGAACACCGGCGGAATCCGGCGTTGCCGCC
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                                         GGCCCCGCCGATGCCGCCTTGGCCGCCGTCACCGCCTTGGCCGCCGGCGCCGCCCTCGCT 3936047
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Sequence 31, Application US/09724797

Patent No. 6733998

GENERAL INFORMATION:

APPLICANT: Jon S. THORSON

APPLICANT: Jon S. THORSON

TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES

TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF

TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE

FILE REFERENCE: 2653-40

CURRENT APPLICATION NUMBER: US/09/724,797

CURRENT FILING DATE: 2000-11-28

CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/111,325
PRIOR FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3935884 GTCGCCGGCCCGCCGCCGCCGCCGCCGCCCCC-----GCCGATACCGGCGTT 3935831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ValArgThrGlyMetAlaAlaGluLeuAlaAlaHisAlaProGlyValGlnHisValGly 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 AlaCysLeuValGlyAspValThrAlaProGlyProGluLeuAlaAlaAlaLeuArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaSerAlaArgArgAlaLeuAla---GluAlaLeuArgSerPheAlaAlaLeuValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgArgLeuMetGlyProGluLeuAlaAla 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGACCCCGCCTTGGCCGCCTTGGCCGCCGAAGCCGTTGCCGTCTTGGGAAGAGGGC 3935276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGCCGCCCGGCCCCGGCCCCGCCGGTGCCGCCGATCCCGCCGGTCGCCGGGAACACC 3935516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGCCGCCGGCCCGGCCCCGCCGTTGCCGCCGTCACCGCTGGCGGCGCTGGCTAG 3935669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCGCGGTTCCGCCGGTGTTGGCCAGGCCGACGCC------GGCGTCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GGTGCTGTTCAGGCCGCCTTTGCCGCCTTGGCC 3935633
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; LOCATION: (1)...(1362)
US-09-724-797-31
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SEQ ID NO 31
LENGTH: 1362
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ORGANISM: Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 ThrGlyArgProValAlaAlaValValThrArgAspGlyProGlyValThrAlaLeuLeu
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nArgSerAsnPro-----ArgAlaAlaSerAlaArgArgAlaLeuAlaGluAlaLeuAr 248
                                                                                                                                                                           AlaArgLeuGlyValAspValArgAlaLeuAlaAlaThr-AlaProProProHisGlnVa
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                                                                                                                                                                                                                                                                         ThrThrAlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAlaLeu 190
                                                                                                                                                                                                                                                                                                                      CCGGTGGTGGGTGGGTGCGGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGCCGCGGCGCCGAGGTGGTCGCGGTCGAC----AGCGACCCGGGCACCGTCGCG
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                                                                                     lLeuLeuAlaLeuLeuAlaArgValLeuGlyGlySerProGluValTyrGlyAspIleGl
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                                               - AGCTCGCGACCAACTGGTGGATCGACGCGAACGT - - GGCGATCGCCA
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Matches:
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APPLICANT: Rea, Stephen
TITLE OF INVENTION: Chromatin-Regulator Genes
FILE REFERENCE: 0652.1670001
CURRENT APPLICATION NUMBER: US/09/589,892B
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 08/945,988
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: PCT/EP96/01818
PRIOR FILING DATE: 1997-05-02
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR FILING DATE: 1996-05-02
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR FILING DATE: 1995-05-10
NUMBER OF SEO ID NOS: 21
COUNTMER: DECETTA VICTOR OF THE PRIOR FILING DATE: 1995-05-10
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                                                                                          US-10-089-514-6 (1-322) x US-09-589-892B-3 (1-2732)
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                                                                                                                                                           Query Match:
                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2 SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jenuwein, Thomas
APPLICANT: Laible, Gotz
APPLICANT: O'Carroll, Donal
APPLICANT: Eisenhaber, Frank
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: 3'UTR
LOCATION: (1284)..(2732)
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LOCATION: (1)..(44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 gSerPheAlaAlaLeuValGlyAspAspProAspArgAlaAspAlaProGlyArgAlaAs
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                               ValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAlaGly
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	49 884	GlyAspValThrAlaProGlyProGluLeuAlaAlaAlaLeuArgAspAlaAspLeuVal 68
	69	LeuLeuAlaValHisGluAspValAlaLeuLysAlaValAlaProValThrArgLeuMet 88
	848	GCTGTTCTTGCGAATCTTCTCCAGGGTGCGGACGCCCAGCCACGCCCATCATC 795
	89	ArgProGlyAlaLeuLeuAlaAspThrLeuSerValArgThrGlyMetAlaAla 106
	794	CGTCCGGAAGATGCAGAGGTCATATCGGATACCCTTCTGTACCACACGATTTGGGCA 738
	107	GluLeuAlaAlaHisAlaProGlyValGlnHisValGlyLeuAsnProMetPheAlaPro 126 :::
	737	GTCATAGCCGCAGCGGCAGCGGGAGTTGCACTCGTAGATGGGCAGCCCGGGCTCGAAGCCG 678
	127	ArgAradlaGlyMetThrGlyArgProValAlaAlaValVal 139
	677	CACCTGGCCCTGGTCATTGTAGGCAAACTTGTGCAGTGACGCCCCCGGGCAGCAGCCTCC 618
	140	ThrArgAspGlyProGlyValThrAlaLeuLeuArgLeuValGluGlyGly 156
	157	GlyGlyArgProValArgLeuThrAlaGluGluHisAspArgThrThr 172
	557	GCCCTCACCAACACGGTACTCATTGATGTACACGAAGGCCCGCGG 513
	173	AlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArg 192
	512	AGGGCCGTCCAGGTCCACCTCATTCTCTACAGTGATGCGTCCCAGATGGCTGCG 459
	193	LeuGlyValAspValArgAlaLeuAlaAlaThrAlaProProProHisGlnValLeuLeu 212
	į	
	213	AlaLeuLeuAlaArgValLeuGlyGlySerProGluValTyrGlyAspIle-GlnAr 231
	410	GGCCTTCTGCACCAGGTAGTTGGCCAAGCTTGGGTCCAGGTGCCGGGGGGGTCTTTGACCG 351
	231	gSerAsnProArgAlaAlaSerAlaArgArgAlaLeuAlaGluAlaLeuArg 248
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-Q-/cgn2 1/USPTO, Spool h/US10089514/runat_04102005 105745 8055/app_query.fasta_1.1621
-DB=Published_Applications_NA -QFMT=fastap__SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS_bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10089514 @CON 1 1 920 @runat 04102005 105745 8055
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 969
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ORGANISM: Streptomyces
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LOCATION: (1)..(966)
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                                                                                 GCGGCGACGGCCGCCCCACCAGGTGCTCGCCCTCCTGGCCCGTGTGCTCGGC
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CGGGCGCTCGCCGAGGCCCTGCGCTCCTTCGCCGCGCTGGTCGGCGACGACCCGGACCGT
                                         GGCAGCCCCGAGGTGTACGGGGACATCCAGCGGTCCAACCCCCGGGCGCGTCCGCGCGC
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FILE OF INVENTION IN VIVO INCORPORATION OF FILE REFERENCE: 54-000120US CURRENT APPLICATION NUMBER: US/10/126,927; CURRENT FILING DATE: 2002-04-19 PRIOR APPLICATION NUMBER: US 60/285,030 PRIOR FILING DATE: 2001-04-19 PRIOR APPLICATION NUMBER: US 60/285,514 PRIOR FILING DATE: 2001-04-19 PRIOR APPLICATION NUMBER: US 60/355,514 PRIOR FILING DATE: 2002-02-06 NUMBER OF SEQ ID NOS: 79 SOFTMARE: Patentin version 3.1 SEQ ID NO 68 LENGTH: 3305 TYPE: DNA ORGANISM: Streptomyces venezuelae US-10-126-927-68
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Publication No. US200300082575A1
GENERAL INFORMATION:
APPLICANT The Scripps Research Instit
APPLICANT Schultz, Peter G
APPLICANT Schultz, Peter G
APPLICANT Hoderson, John C
APPLICANT Liu, David R
APPLICANT Liu, David R
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                                                      GlyArgProAspAlaCysLeuValGlyAspValThrAlaProGlyProGluLeuAlaAla
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RESULT 3
US-10-126-927-67
; Sequence 67, Application US/10126927
; Publication No. US20030082575A1
; GENERAL INFORMATION:
APPLICANT: The Scripps Research Instit
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Anderson, John C
APPLICANT: Liu, David R
APPLICANT: Liu, David R
APPLICANT: Magglery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Meggers, Eric L
APPLICANT: Meggers, Eric L
APPLICANT: Meggers, Miro
APPLICANT: Pastrnak, Miro
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NT: Pastrnak, Miro
NT: Santoro, Stephen
NT: Zhang, Zhiwen
F INVENTION: In Vivo Ir
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; TYPE: DNA
; ORGANISM: Plasmid
US-10-126-927-67
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SOFTWARE: PatentIn versionsEQ ID NO 67
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CURRENT APPLICATION NUMBER: US/10/126,927
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
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Indels:
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US-10-137-310-3
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SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 1122
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APPLICANT: Witsky, Timothy A.
APPLICANT: Mitsky, Timothy A.
TITLE OF INVENTION: Tyra Genes and Uses Thereof
FILE REFERENCE: 16515.147
CURRENT APPLICATION NUMBER: US/10/137,310
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/289,527
PRIOR FILING DATE: 2001-05-09
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ORGANISM: Escherichia
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 GluLeuAlaAlaHisAlaProGlyValGlnHisValGlyLeuAsnProMetPheAlaPro
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                                                                                        MetArgProGlyAlaLeuLeuAlaAspThrLeuSerValArgThrGly---MetAlaAla
                                                                                                                                                          ValLeuLeuAlaValHisGluAspValAlaLeuLysAlaValAlaProValThrArgLeu
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Best Local Similarity:
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US-10-433-556-18
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                                                    US-10-089-514-6 (1-322) x US-10-433-556-18 (1-1122)
                                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 1122
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/433,556
CURRENT FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Matringe, Michel
APPLICANT: Rippert, Pascal
TITLE OF INVENTION: Novel Targets For
TITLE OF INVENTION: Said Herbicides
FILE REFERENCE: 5500*120
                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                            No.:
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ValValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAla
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Matches:
Conservative:
Mismatches:
Indels:
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-ArgArgAlaLeuAla

900 223 840 203

239

183 720 163 660

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1020 244 960

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US-10-380-132-7
APPLICANT: SunGene GmbH & Co. KGaA
TITLE OF INVENTION: Improved processes for vitamin
FILE REFERENCE: NAE445/2000
CURRENT APPLICATION NUMBER: US/10/380,132
CURRENT FILING DATE: 2003-03-11
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 1238
TYPE: DNA
                                                                                                                                                                                                    Sequence 7, Application US/10380132 Publication No. US20030182679A1 GENERAL INFORMATION:
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LOCATION: (1233)..(1238)
OTHER INFORMATION: restriction
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NAME/KEY: CDS
LOCATION: (25)..(1143)
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LOCATION: (7)..(1232)
OTHER INFORMATION: mutase / prephenate dehydrogenase
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Sequence 1, Application US/10137310

Publication No. US20030176675A1

GENERAL INFORMATION:
APPLICANT: Valentin, Henry E.
APPLICANT: Mitsky, Timothy A.
TITLE OF INVENTION: TyrA Genes and Uses Thereof
FILE REFERENCE: 16515.147

CURRENT APPLICATION NUMBER: US/10/137,310
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/289,527
PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0

SEQ ID NO 1
LENGTH: 1122
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ORGANISM: Erwinia
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LENGTH: 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valentin, Henry E.
APPLICANT: Venkatesh, Tyamagondlu V.
APPLICANT: Venkatesh, Tyamagondlu V.
APPLICANT: Venkatesh, Tyamagondlu V.
FILE OF INVENTION: Tocopherol biosynthesis related genes and used thereof FILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: US 60/400,689
PRIOR FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
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                                   48 ValGlyAspValThrAlaProGlyProGluLeuAlaAlaAlaLeuArgAspAlaAspLeu 67
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                                                                                                                    GlySerArgThrLeuValValAspLeuValProProProGlyArgProAspAlaCysLeu
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-----AAAGAGGACTGGCCTCAGGCTGAGACTCTGCTCAGCGATGCCGGAATG
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Hirshberg, Joseph
Karunanandaa, Balasuloji
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; ORGANISM: Erwinia l
; FEATURE;
; NAME/KEY: CDS
; LOCATION: (1)..(11)
US-10-433-556-20
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-433-556-20
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                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 5500*120
CURRENT APPLICATION NUMBER: US/10/433,556
CURRENT FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matringe, Michel
APPLICANT: Rippert, Pascal
TITLE OF INVENTION: Novel Targets For
TITLE OF INVENTION: Said Herbicides
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                             ValValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAla
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                                              Sequence 1, Application US/10329670
Publication No. US20040018503A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome,
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,670 CURRENT FILING DATE: 2002-12-24 PRIOR APPLICATION NUMBER: US 09/643,990
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                                                                                                                                                                                                                                                                               AlaAspAlaPro----
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PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
'COCATION: (45593)..(45593)
'COCATION: n equal
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NAME/KEY: misc_feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
1001. (9921)...(992)
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NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
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ORGANISM: Haemophilus influenzae
                      NAME/KEY: misc feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
                                                                    NAME/KEY: misc_feature
LOCATION: (47036)...(47036)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER_INFORMATION: n equals
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals
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LOCATION: (36543)..(36543)
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OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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LOCATION: (44416)..(44416)
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APPLICATION NUMBER: US 08/487,429
FILING DATE: 1995-06-07
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (100091)...(100091)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equal
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equal
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OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (51786)..(51786)
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                                                                              LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (65313)..(65313)
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Best Local Similarity:
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LOCATION: (152530)..(152530)
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LOCATION: (152500)...(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
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LOCATION: (145942)..(145942)
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AlaProValThrArgLeuMetArgProGlyAlaLeuLeuAlaAspThrLeuSerVal---
                                 TTAGCGAATGCTGATCGTGATCGTTCCGTCCTATTAATCTCACCTTAGAAACAATT
                                                                                CGCGAAGATTGGGCGGTGGCTGAAAGTATT-----
                                                                                                                           CGTTATTTACGTGCATCTGGCTATCCAATTTCTATTTTAGAT-----
                                                                                                                                                 GlyLeuLeuArgGluAlaGlySerArgThrLeuValValAspLeuValProProProGly
                                                                                                     ArgProAspAlaCysLeuValGlyAspValThrAlaProGlyProGluLeuAlaAlaAla
                                                                                                                                                                       TCTGATATTCACAAAATTGTTATTGTGGGCGGTTATGGTAAATTAGGCGGCTTATTTGCC 1370798
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US-10-158-865-1
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Publication No. US20040203093A1
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide Sequence of the TITLE OF INVENTION: Thereof, and Uses Thereof FILE REFERENCE: PB186P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                               LENGTH: 18
TYPE: DNA
                                                                                                  NAME/KEY: misc feature
LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
                              NAME/KEY: misc feature LOCATION: (10150)..(10
                                                                                                                                                                                                               OTHER INFORMATION: n equals
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                                                                                    FEATURE:
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FEATURE:
NAME KEY: misc feature
LOCATION: (47036)...(47036)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (65313)..(65313)
OTHER_INFORMATION: n equals
                                                  NAME/KEY: misc_feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51786)...(51786)
OTHER_INFORMATION: n equals
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LOCATION: (44975)...(44975)
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LOCATION: (44905)..(44905)
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LOCATION: (44416)..(44416)
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LOCATION: (36636)..(36636)
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LOCATION: (36551)..(36551)
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LOCATION: (29298)..(29298)
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equal
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LOCATION: (51805)..(51805)
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LOCATION: (51334)..(51334)
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LOCATION: (40808)..(40810)
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LOCATION: (36543)..(36
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LOCATION: (45593)..(459
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NAME/KEY: misc feature
LOCATION: (121344)...(121344)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER_INFORMATION: n equals
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (122167)..(1:
OTHER INFORMATION: n ed
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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
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NAME/KEY: misc_feature
LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
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LOCATION: (140398)..(14
OTHER INFORMATION: n ed
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(1
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LOCATION: (120038)..(120038)
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)...(150841)
OTHER INFORMATION: n equals
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LOCATION: (147197)...(147197)
OTHER_INFORMATION: n'equals a,t,
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OTHER INFORMATION: n equals
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                                                                                                             ATTTATCAAACCAATGCCACAGAACACGATCATAATATGACTTATATACAAGCCTTGCGC 1371224
                                                                                                                                                                                                                                                               CATCCAATGTTTGGTGCAGATATTGCAAGTATGGCAAAACAAGTGGTTGTGTGCGTTGTGAT 1371104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuArgAspAlaAspLeuValLeuLeuAlaValHisGluAspValAlaLeuLysAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuLeuArgGluAlaGlySerArgThrLeuValValAspLeuValProProProGly 41
LeuAlaAlaThrAlaProProProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeu 219
                                       CATTTTTCGACTTTTGCGAATGGTTTACACCTTTCCAAACAGCCCATTAATCTCGCTAAT 1371284
                                                                                                                                                                                     GGACGTTTTCCTGAACGTTATGAATGGTTACTTGAGCAAATTCAAATTTGGGGTGCAAAA 1371164
                                                                                                                                                                                                                                                                                                   AsnProMetPhe---AlaProAlaAlaGlyMetThrGlyArgProValAlaAlaValVal 139
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                                                                          HisAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAla
                                                                                                                                                ProValArgLeuThrAlaGluGluHisAspArgThrThrAlaAlaThrGlnAlaLeuThr 179
                                                                                                                                                                                                                        ThrargaspGlyProGlyValThralaLeuLeuArgLeuValGluGlyGlyGlyGlyArg 159
                                                                                                                                                                                                                                                                                                                                          CGTGAACCGCTAGCGAAAATGCTTGAAGTTCATACTGGTGCTGTT-----TTAGGTTTA 1371044
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CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US 10/158,865
PRIOR PLING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEO ID NOS: 1
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Publication No. US20050131222A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fra-
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P2C1D12
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           NAME/KEY: misc_feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
                                                                                     NAME/KEY: misc_feature
LOCATION: (36636)..(36636)
OTHER_INFORMATION: n equals
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LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (9921)..(992
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NAME/KEY: misc_feature
LOCATION: (4747)..(474
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LOCATION: (29298)..(29298)
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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FEATURE:
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NAME/KEY: misc feature
LOCATION: (107248)...(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)...(100091)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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LOCATION: (65313)...(65313)
OTHER INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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LOCATION: (51786)...(51786)
OTHER INFORMATION: n equals
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals
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LOCATION: (47036)...(47036)
OTHER_INFORMATION: n equals
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER_INFORMATION: n equals
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LOCATION: (44975)...(44975)
OTHER INFORMATION: n equals
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER_INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145171) .(145171)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360) ... (131360)
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (145058)..(14
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OTHER INFORMATION: n equals
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Best Local Similarity:
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 Sequence 1605, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACI
FILE REFERENCE: 790CIP3/US
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CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUStom
SEQ ID NO 1605
LENGTH: 1792
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (567)...(4)
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                                                                                                                                 GluHisAspArgThrThrAlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPhe 186
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ProHisGlnValLeuLeuAlaLeuLeuAlaArgValLeuGlyGlySerProGluValTyr 226
                                 GGGCTGCACCTGGCAGAAGAAAATGTTCAGCTTGAGCAACTTCTGGCGCTCTCTTCGCCG
                                                                GlyLeuAlaLeuAlaArgLeuGlyValAspValArgAlaLeuAlaAlaThrAlaProPro
                                                                                                 GAGCACGATCAGAATATGGCGTTTATTCAGGCACTGCGCCCACTTTGCTACTTTTGCTTAC
                                                                                                                                                                       CAATGGTTTCTGGAGCAAATTCAGGTCTGGGGCGCTCGGCTGCATCGTATTAGCGCCGTC
                                                                                                                                                                                                     -----LeuLeuArgLeuValGluGlyGlyGlyArgProValArgLeuThrAlaGlu 166
                                                                                                                                                                                                                                         AGCCTGGCAAAGCAAGTT-----GTGGTCTGGTGTGATGGACGTAAACCGGAAGCATAC
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US-10-297-465A-1/c
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SOFTWARE: PatentIn vers
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LENGTH: 2731748
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APPLICANT: Arruda, Paulo
TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and
FILE REFERENCE: FAPESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465A
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: PCT/IB01/01618
PRIOR APPLICATION NUMBER: PCT/IB01/01618
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR FILING DATE: 2001-06-17
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APPLICANT: Reinach, Fernando
APPLICANT: Setubal, Joao
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ORGANISM: Xylella
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                                       US-10-089-514-6 (1-322) x US-10-369-493-37621 (1-2025)
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                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 37621
LENGTH: 2025
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION UNMERS: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas fluorescens
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  8 ValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAla 27
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                                                                                                                                                                                                                                                                      724 TGGCATGACATCTTTCTCGCCAAC-------CGCGAGGCTGTCCTGCGC 765
                                                                                                                                                                                                                                                                                                    226 TyrGlyAspIleGlnArgSerAsnProArgAlaAlaSerAlaArgArgAlaLeuAlaGlu 245
                                                                                                                                                                                                                                                                                                                                             679
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                                                                                                                                                                                                                                                                                                                                                                                                                                          188 Leu-----AlaLeuAlaArgLeuGlyValAspValArgAlaLeuAlaAlaThrAlaPro 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 CACGATGAAGTGCTGGCCGCACCATCTGCCGCAC-----CTGCTGGCCTTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 HisAspArgThrThrAlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGly 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 LeuLeu---ArgLeuValGluGlyGlyGlyGlyArgProValArgLeuThrAlaGluGlu 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 TTCCGTCGTCATAAAGTGATTCTGACCCCGTTGGAGCAGCCGATCCGGCCGCCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 GIGCGIGCGGCGACCGAAGCGTICGGC------GGCAIGCCGGCGCGCGTTICGIG 384
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                                                                                                  286 PheGlyGluLeuArg 290
                                                                                                                                                                    266 ArgAlaAspAlaProGlyHisProGlyGlyCysAspGlyAlaGlyAsnLeuAspGlyVal 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 ProAlaAlaGlyMetThrGlyArgProValAlaAlaVal------------ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AlaGluLeuAlaAlaHisAlaProGlyValGlnHisValGlyLeuAsnProMetPheAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GTCGAGTTGGGCGTGGATCGTTGCGAAGACGACCTGGTGGCGGCTTGCCGGGGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ArgLeuMetArgProGlyAlaLeuLeuAlaAspThrLeuSerValArgThrGlyMetAla 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                     ACACTCGATACATTTCGCAGCGACCTCGACGCCTTGCGCGACGCGGTCGATGCA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspLeuValLeuLeuAlaValHisGluAspValAlaLeuLysAlaValAlaProValThr 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gly---SerArgThrLeuVal---ValAspLeuValProProProGlyArgProAspAla 45
                                                                                                                                     ------GGGGATGGGCAC-----
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(Ołdzu) Mnola Blonk (uspło)

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-MODBLE frame+ p2n.model -DEV=x1h
-Q=/cgn2 1/USPTO_spool_h/US10089514/runat_04102005_105744_8043/app_query.fasta_1.1621
-Q=/cgn2 1/USPTO_spool_h/US10089514/runat_04102005_105744_8043/app_query.fasta_1.1621
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10089514 @CGN_1 1.6050 @runat_04102005_105744_8043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AUTHORS RESULT 1 AG020402/c VERSION KEYWORDS FEATURES REFERENCE SOURCE ACCESSION DEFINITION POCUS ORGANISM JOURNAL TITLE AUTHORS Submitted (16-OCT-1999) Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato University; 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:81-42-778-9923, Fax:81-42-778-9924) Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA, chromosome 21q Published Only in Database (1999)

2 (bases 1 to 597) Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y. Eukaryota; Metazoa; Chordata; Crániata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Homo sapiens genomic DNA, genomic survey sequence. Direct Submission AG020402.1 Homo sapiens (human) AG020402 AG020402 /map="21q" /clone="B53P19_BB042(Fw).ab1" /organism="Homo sapiens"
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                                                                                                             Homo
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA, chromosome 21q Published Only in Database (1999)
                                                                                                                                                                          Homo sapiens genomic DNA, genomic survey sequence. AG020403
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                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                            Homo sapiens (human)
                                                                                                                                                             AG020403.1 GI:6046347
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Location/Qualifiers
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Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A.,
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
Direct Submission
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                               TCTTCGCCGATTTACCGCCTTGAGCTGGCGATGGTC
                                                                                           TTTGCTTACGGGCTGCACCTGGCAGAAGAAAATGTTCAGCTTGAGCAACTTCTGGCGCTC
                                                                                                                       LeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAlaLeuAlaAlaThr
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/map="21q"
/clone="853p19_BB042(Rv)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags Unpublished (2003)
Other_ESTs: EST701086
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CF823705
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EST701087 Coccidioides posadasii saprobic phase cDNA library,
4 kb Coccidioides posadasii cDNA clone CIDAN17 5' end, mRNA
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
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SerValArgThrGlyMetAlaAlaGluLeuAlaAla------
                                                                                                                       GTCTCC-----AGAGTTAGCGACTACATTATCTACAGTGTAGAGGCAGAAGCCATCAAC
                                                                                                                                                       AlaAlaAlaLeuArgAspAlaAspLeuValLeuLeuAlaValHisGluAspValAlaLeu
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                                                     AAAATTGTGGCGGAGTATGGCCCATCAACCAAAGTTGGCGCGATTGTTGGTGGTCAAACT
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                                                                                     LysAlaValAlaProValThrArgLeuMetArgProGlyAlaLeuLeuAlaAspThrLeu
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/lab_host="E. coli DH10B, Tl phage resistant"
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library, 2 to 4 kb"
/note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"
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/mol_type="mRNA"
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/clone="CIDAN17"
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Eukaryota; Fungi; Ascomycota; Peżizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 875)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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EST818210 Coccidioides posadasii saprobic phase cDNA library,
greater than 4kb Coccidioides posadasii cDNA clone CIBCR06 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: gardner@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 3519 Fax: 301 838 0208
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                                                                                                                                                                                                                                                  /dev_stage="saprobic phase (mycelia)"
/lab host="E. coli DH10#, T1 phage resistant"
/clome lib="Coccidioides posadasii saprobic phase cDNA
library, greater than 4kb"
/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii approbic phase cDNA library, size
fractionated cDNA > 4 kb"
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/strain="C735"
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/clone="CIBCR06"
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Tel:
                                                                                                                                                                                             Other ESTs: EST791780
Contact: Gardner MJ
The Institute for Genomic Research
The Medical Center Drive, Rockvil
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Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags
Unpublished (2003)
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301 838 0208
                                                                                                                                                          gardner@tigr.org
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0.4 to 2.3 kb"
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                                        cr823364
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posadasii
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/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV Coccidioides posadasii spherule cDNA library, 0.4 to 2.3 kb"
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CF823364 900 bp mRNA linear EST 01-APR-2004 EST700746 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAL10 5' end, mRNA
                                                                                                                                                    ----TAAGCGCAGAGTCAAGGCTGCCAGGGCGGCTGT
                                                                                                                                                                                                AspAlaProGlyArgAlaAspAlaProGlyHisProGlyGlyCys
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 900)
Gardner, M.J. and Cole, G.T.

Analysis of gene expression in Coccidioides posadasii mycelia spherules via expressed sequence tags
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: gardner@tigr.org
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: EST700745
Contact: Gardner MJ
CAATTCCCGTGGGAGATATCTCGATATGTGGGTGGAATTGAA----
                                                                                               ThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAla------
                                                                                                                                TCTTTCGAATCCAAATACGTTTACCTCACCGGGGAGAGGCATGATCGAATCACAGCGGAC 466
                                                                                                                                                     GlyGlyGlyArgProValArgLeuThrAlaGluGluHisAspArgThrThrAlaAla 174
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                                                                ACTCAGGCCGTGACGCATGCTGCATTTTTGAGTATGGGAACTGCGTGGCAAGCCCAATAAC 526
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2 Medical Center Drive, Rockville,
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301 838 0208
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/lab_host="E. coli DH10B, T1 phage resistant"
/clone lib='Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb" posadasii saprobic phase cDNA
/note='Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"
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/clone="CIDAL10"
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AUTHORS
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ORGANISM
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KEYWORDS
                                                                       US-10-089-514-6 (1-322) x CF881643
                                                                                                                                    Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           North Carolina State University Campus Box 7251, Raleigh, NC 27 Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K., Ward, M. and Dean, R.A.
Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Ralph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 973)
Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ralph_dean@ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 919-513-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungal Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEMS Microbiol Lett 230
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GlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAlaGlySerArgThr
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                        /note="Vector: pREP3Y; $ite_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Car and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                   /dev stage="mycelia"
/clone_lib="T.reesei mydelial culture, Version
2003"
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
                                                                                                                                                                                                                                                                                                                                                                                                            clone="tric028xo14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Hypocrea
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30.10%
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremel
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CCAHL63TR C.neoformans strain JEC21 Cryptococcus neoformans
neoformans cDNA clone CCAHL63, mRNA sequence.
                                                                                                                                                     Department of Eukaryotic Rockville, MD 20850, USA Tel: 301-838-3543
                                                                                                                                                                                                                          Unpublished (2003)
Other_ESTs: CCAHL63TF
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EST.
                                                                                                             Seq
                                                                                                                          Email: crypt@tigr.org
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                                                                                                                                                                                                             Contact: Brendan Loftus
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                                                                                j. .821
                                        /mol_type="mRNA"
/strain="JEC21"
                                                        /organism="Cryptococcus
/mol_type="mRNA"
                                                                                              Location/Qualifiers
            b_xref="taxon:40410"
lone="CCAHL63"
 _lib="C.neoformans
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> /note="Vector: pCMVSport6; Site_1: NotI EcoRV; The length, normalized library was prepared from a vari conditions using RNA provided by Joseph Heitman and Jennifer Lodge" a variety man and full of f

Percent Similarity: Best Local Similarity: US-10-089-514-6 (1-322) x CF682058 27 AlaGlySerArgThrLeuValValAspLeuValProProProGlyArgProAspAla---GCTGAACCCGTCGGCCAAATCC gSerAsnProArgAlaAlaSer 238 uLeuAlaLeuLeuAlaArgValLeuGlyGlySerProGluValTyrGlyAspIleGlnAr Arg-LeuGlyValAspValArgAlaLeuAlaAlaThrAlaProProProHisGlnValLe ACTGCCAACACCCCAGGCTGTGACGCATGCGGCTTTCCTCAGTATGGGTACAGCATGGCAG ThrAlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAlaLeuAla GTTTTTAGGTCATTCAAGAGTCGATACGTTCATCTGAGCTACGAAGAGCATGATAAAGTG LeuValGluGlyGlyGlyArgProValArgLeuThrAlaGluGluHisAspArgThr CCGCTT----ATTATCATACATCACAGAGGTCCGGAAGAGATGTGAAGATGGTTGAAGAT ProValAlaAlaValValThrArgAspGlyPro-----GlyValThrAlaLeuLeuArg GATGTGGGGATTACGAGTGTACATAGTTTGCATGGGCCGAGTGTGACGACAGAGGGCCAG HisValGlyLeu-----AsnProMetPheAlaProAlaAlaGlyMetThrGlyArg CAGACGAGTGTGAAAGCCCCCGGAGAGGGGAGGGCATTTGAGAGATGGTTACCG-----GAG ThrLeuSerValArgThrGlyMetAlaAlaGluLeuAlaAlaHisAlaProGlyValGln GTCTCGCGTCTTTCCACATTCATCATTTATTCTGTC---GAAGCTGCTGCGTTGCCGGCT AlaLeuArgAspAlaAspLeuValLeuLeuAlaValHisGluAspValAlaLeuLysAla GAGGCCCTCGAGGAAGAATTCAAAGGGACCGGCATACATGTCCTCCGCAACGGTCACGCC ---CysLeuValGlyAspValThrAlaProGlyProGluLeuAla------Ala GGCGGCATCGAGACTATCTACGTC-----GTGGTAGGCATCATCGGGATGGGTGATATGGGACGGATGTATGCAAAGCGATTACATGCG ValValGly-----GlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGlu GGTCAACATTACCCTCCGTATCTACTCTGCCAAATGGCACGTCTACGCCGGTCTTGCGCT AAATCTTCATCTTACCCATGGGAAACTACGCGCTACGTGTCCGGTATC-GAAGTGATCAA -----AlaProValThrArqLeuMetArgProGlyAlaLeuLeuAlaAsp 830 bp mRNA linear C.neoformans strain JEC21 Cryptococcus cDNA clone CCAHK69, mRNA sequence. 0.00903 146.50 43.55% 29.03% 8.96% (1-821)780 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: ----TGCGACAAACCCGACTCTTTC 821 72 36 110 31 neoformans EST 16-AUG-2004 758 869 639 191 579 519 462 133 402 116 348 96 80 60 180 45 26 211 151 297 240

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Heterobasidiomycetes; Tremellomycetidae; Tremel
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Other_ESTs: CCAHK69TF
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  HisValGlyLeu-----
                                                                                                                                                                                             Val-----AlaProValThrArgLeuMetArgProGlyAlaLeuLeuAlaAsp
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                                                                 CAGACGAGTGTGAAAGCCCCCGGAGAGGGGAGGCATTTGAGAGATGGTTACCG-----GAG
                                                                                                            ThrLeuSerValArgThrGlyMetAlaAlaGluLeuAlaAlaHisAlaProGlyValGln 116
                                                                                                                                                       GTCGTGAGAGAGTACGGACCTTCGACTCGGGTG---
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/clone="CCAHK69"
/clone_lib="C.neoformans strain JEC21"
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Tel: 301 838 3519
Fax: 301 838 0208
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Other_ESTs: EST697173
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Gardner,M.J. and Cole,G.T.
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Location/Qualifiers
                                                                                                                                                                                       /dev stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb"
/note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
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/strain="C735"
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 Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, I
Tel: 86-10-80481559
                                                                             Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan, Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice gen its comparison to Arabidopsis
                                                                                                                                                                           Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Cyza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1407)
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Class: exon-trapped.
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Email: chenchen@genomics.org
rProGluValTyrGlyAspIleGlnArgSerAsn--
                                                                                                                                      lLeuLeuSerPheGlyLeuAlaLeuAlaArgLeuGlyValAspValArgAlaLeuAlaAl
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/mol type="genomic DNA"
/db xref="taxon:3946"
/clone_lib="Oryza sativa E
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AG061086
AG061086.1 GI:10
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asso Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-917B) This BAC encorate derived from the chimpanzee BAC library PTB This BAC encorate generated during the R&D process and may have higher chance of
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Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y
BAC end sequences of Library PTB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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.Site 1 : SacI
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                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                        clone="PTB-049A11.F"
                                                                                                                                                                                                                                           sex="male"
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nd Sakaki, Y.
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                Clark, A.G., Glanowski, S
Todd, M.A., Tanenbaum, D.
Ferriera, S., Wang, G., Z
                                                                                                                                      1 (bases 1 to 1086)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                 gene trios
Science 302
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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                  AlaLeuLeuAlaArgValLeuGlyGlySer---ProGluValTyrGlyAspIle-GlnAr
                                                                                                            AGGGCCGTCCAG-----GTCCACCTCATTCTCTACAGTGATGCGTCCCAGATGGCTGCG
                                                                                                                                     AlaAlaThrGlnAlaLeuThrHisAlaValLeuLeuSerPheGlyLeuAlaLeuAlaArg
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GGCCTTCTGCACCAGGTAGTTGGCCAAGCTTGGGTCCAGGTGCCGGGGGGTCTTTGACCG
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                                                                                 LeuGlyValAspValArgAlaLeuAlaAlaThrAlaProProProHisGlnValLeuLeu
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/mol_type="genomic DNA"
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                               9 ValValGlyGlySerGlyAlaValGlyGlyMetPheAlaGlyLeuLeuArgGluAlaGly
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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2 (bases 1 to 1684)
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/tissue_type="B_cells (Ramos
/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                               Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Pan troglodytes DNA, clone:
AG071167 GI:16622969
GSS.
                                                                                                                                                                                     was generated during the R&D process and may have higher chance
                                                                                                                                                                                                 Clones are derived from the chimpanzee BAC library PTB This BAC
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Totoki, Y., Watanabe, H. and
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Mammalia; Eutheria; Primates;
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                                                                                                                                     Sequencing: -21M13
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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nd Sakaki,Y.
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                                                             AsnProArgAlaAlaSerAlaArgArgAlaLeuAlaGluAlaLeuArgSerPheAlaAla
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
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